

GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: November 12, 2004, 12:54:14 ; Search time 42 Seconds

(without alignments)
1466.160 Million cell updates/sec

Title: US-10-730-010-2

Perfect score: 3404

Sequence: 1 MKKYDVKAIGQAGFKAYL.....LCANDCSLKDSEKEMELRT 640

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1078	31.7	774	S25284	protein kinase nek
2	659.5	19.4	792	JC7122	protein kinase (EC
3	655	19.2	841	I78885	serine/threonine-s
4	569	16.7	357	T29771	hypothetical prote
5	535.5	15.7	445	G0452	NIMA-like protein
6	520.5	15.3	431	T11854	protein kinase (EC
7	512.5	15.1	699	A43734	probable protein k
8	507.5	14.9	722	T37970	probable G2-specif
9	471.5	13.9	338	JC7838	Nek6 protein kinas
10	459	13.5	779	A57177	NIMA-like protein
11	451	13.2	941	T49136	protein kinase-lik
12	424	12.5	294	T21075	hypothetical prote
13	423	12.4	435	S23580	probable protein k
14	415.5	12.2	200	B96587	hypothetical prote
15	410	12.0	648	T47988	serine/threonine-p
16	405.5	11.9	1895	T15881	hypothetical prote
17	396.5	11.6	114	T13824	protein-serine/thr
18	395.5	11.6	1142	S53359	GIN4 protein - yea
19	394	11.6	925	A55748	protein kinase (EC
20	393.5	11.6	576	S22127	protein kinase pol
21	393.5	11.6	705	A48144	protein kinase CDC
22	393	11.5	465	B55748	protein kinase (EC
23	391	11.5	658	T39500	serine/threonine-s
24	387.5	11.4	1051	JW0051	serine/threonine-s
25	385	11.3	1558	T23253	hypothetical prote
26	384.5	11.3	733	A57459	ribosomal protein k
27	381	11.2	257	G84797	probable protein k
28	381	11.2	461	T14822	probable serine/thr
29	379	11.1	445	T50802	serine/threonine p

30 379 11.1 682 2 A44493 serum-inducible ki
31 377 11.1 490 2 S47946 protein kinase hom
32 376 11.0 915 2 S74283 probable protein k
33 375 11.0 819 2 A53714 protein kinase (EC
34 374.5 11.0 752 1 A32571 ribosomal protein
35 373.5 11.0 608 2 G96575 probable MEK kinas
36 373.5 11.0 856 2 T43631 serine/threonine k
37 372.5 10.9 735 2 T51901 ribosomal protein
38 372.5 10.9 740 2 T24340 hypothetical prote
39 372.5 10.9 797 2 T23927 hypothetical prote
40 372.5 10.9 897 2 S61137 probable membrane
41 371.5 10.9 363 2 T08542 mitogen-activated
42 371.5 10.9 363 2 T51735 mitogen-activated
43 370 10.9 982 2 T18576 serine-threonine k
44 369 10.8 1062 2 S46367 protein kinase CDC
45 368.5 10.8 795 2 JC4234 gene fused protein

ALIGNMENTS

RESULT 1

S25284

protein kinase nek1 (EC 2.7.1.1) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004

C:Accession: S25284

R:Letwin, K.; Mizzen, L.; Motro, B.; Ben-David, Y.; Bernstein, A.; Pawson, T.

EMBO J. 11, 3521-3531, 1992

A:Title: A mammalian dual specificity protein kinase, Nek1, is related to the NIMA cell

A:Reference number: S25284; MUID:93010942; PMID:1382974

A:Accession: S25284

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-774 <LET>

A:Cross-references: UNIPROT:P51954; GB:S45828; NID:g256854; PIDN:AAB23529.1; PID:g256855

C:Genetics:

A:Gene: nek1

C:Superfamily: protein kinase homology

C:Keywords: ATP; phosphotransferase

F:2-259/Domain: protein kinase homology <KIN>

F:10-18/Region: protein kinase ATP-binding motif

Query Match		31.7%	Score 1078;	DB 2;	Length 774;
Best Local Similarity		36.4%	Pred. No. 2.5e-35;		
Matches 260;		Conservative 107;	Mismatches 171;	Indels 176;	Gaps 21;
Qy	1	MDKYDVKAIGQAGFKAYLAKGSKSKHCVCVKEINFEKMPIOEKESKKEVILLERMKH	60		
Db	1	MEKYVRLQKIGEGSGFKAVLVKSTEDGRHYVVIKEINISMSDKEROESREAVLANMKH	60		
Qy	61	PNIVAFNSFOENGRFLFVMEYCDGDLMKRINRQGVLFSEDOILGWFOVISLGLKHII	120		
Db	61	PNIVQYKESFEENGSLYVMDYCEGDLFKRINAQKALFOEQIIDLWFVQICLAKHVF	120		
Qy	121	DRKILHSDIKAQNIFLSKNGWAKLGDGFIARVNNNSMELARTICGTPYYLSPEICQNKP	180		
Db	121	DRKILHSDIKSQNIFLTQGTV-QLGDFGIARVNNNSMELARTICGTPYYLSPEICQNKP	179		
Qy	181	YNNKTDVNSLGVLYELCTLKHPEGNLQOLVLTQAHFAIPISCFSELSLSQLF	240		
Db	180	YNNKSDIWAIGCVLYELCTLKHAFENKMLVKIISGFPFVPSHYSYDLRLSLQLF	239		
Qy	241	QVSPDRPSINSILKRPFFLENLIPKVIITPEVIOEESFHMILICRAG-----	285		
Db	240	KRNPRDRPSVNSILEKFIKRLFKLSPQLIAEEFCLTKLSKFGPQLPKGRPASQGV	299		
Qy	286	-----APASRHAGKVQCKTKQVFRGRCFPRSRIS--VPIKNAILHRNEWRP	333		
Db	300	SSFVPAQKITPKAAKYGVPILTYKKYGDKLLLEKPPPKQAQHIPIVKK---MNSGEERK	356		
Qy	334	PAG--AQKARSIMKIER-----	348		

Db 357 KQSEAAKRRLEFIEKKQKQDIFLKAEQMKRQKQBLERINRAREQGWENVLKAGG 416
QY 349 -----PKIAVCGHYDYVAAQDMLAR-RAH-----KPSYHP--IPQE 393
Db 417 SCEVKASFFGIGGAVSPSPRCQYEHYHAFQMQRLRAEDNEARWKGGIYGRWLPER 476
QY 384 NTG---VEDYQETRHGSPSQWPAEYLORKFAQQVKKLVE-----KOLGLRPS 431
Db 477 QKGLAVARANQ-----VEEFLQRKEAMQKARABGVVYLARLQIRLQ--- 522
QY 432 AEPYNQORQLR-----SNGEPRFOELPFRKMKMEQOEYWKOLEBIRQOYLN 479
Db 523 ---NFNERQIQKAKLRGENKEADTKGQEAAT-BETDMR---LKMESLKQAQTNARAVALK 575
QY 480 DMKIRKMGPEPEDEKDLKQMLQNTKESKNP-----EOKYKAKKGVKF--- 525
Db 576 EQLERKKEAYERE--KKVWEHULVARVKSDDVPLPLELLETGSPSKQKQVKPVSUTSA 633
QY 526 --EINLDCIDENILOEEFAMDIENETLT-----FEDGMKFEYECVKEH 569
Db 634 LKEVLDGSLTD---TQEEEMKSNASISSKREILRLNENLKAQDEKEKQH 683
RESULT 2
JC7122
protein kinase (EC 2.7.1.37) 2 - mouse (strain balb/c)
N:Alternate names: serine (threonine) protein kinase
C:Species: Mus musculus (house mouse)
C:Accession: JC7122
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
R:Hayashi, K.; Igarashi, H.; Ogawa, M.; Sakaguchi, N.
Biochem. Biophys. Res. Commun. 264, 449-456, 1999
A:Title: Activity and substrate specificity of the murine STK2 serine/threonine kinase
A:Reference number: JC7122; MUID:20001940; PMID:10529384
A:Accession: JC7122
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-792 <HAY>
A:Cross-references: UNIPROT:Q9Z1J2; GB:AJ233071; NID:94138208; PID:94138209
C:Keywords: human serine/threonine-specific protein kinase STK2; protein kinase homol
C:Superfamily: human serine/threonine-specific protein kinase STK2; protein kinase homol
C:Keywords: phosphotransferase

Query Match 19.4%; Score 659.5; DB 2; Length 792;
Best Local Similarity 29.5%; Pred. No. 4.5e-19;
Matches 157; Conservative 108; Mismatches 161; Indels 107; Gaps 14;
QY 4 YDVVKAIGGAFGKAYLAKGSDSKHCVIKTEINFEKMPIOKEASKKEVILLKMKHPNI 63
Db 6 YCYMRVGRSGYGEVTLVKHRDQKQYVVKLNLRNASSRRRAAEQAQLLSQKHPNI 65
QY 64 VAFNFSFO-ENGRLFIYMEYCDGDLMKRINRQGVLFSEDIQLGFWFVQISLGLKHIHDR 122
Db 66 VTYKESWEGDGLLYVMGFCEGGDLVYKLEQKQQLLPESQVVEFWQIAVALQYLHEK 125
QY 123 KILHRDIAQNIIFLSKNGWAKLGDGFIARVLNNSMELARTCIGTPYVLSPEICONKPNY 182
Db 126 HILHRDLTKQNVFLRTNII-KVGDGLIARVLEHNDMASTLIGTPYVMSPELFSNKPYN 184
QY 183 NKTIDWSLGCVLVELCTLKHDPFEGNNLQQLVLCQAHFAPISPGFSRELHSLISQLFQV 242
Db 185 YKSDVWALGCCVYEWATLKHAFNAKMNSLVYRIIEGKLPMKPVYVSTELAEILRTLSR 244
QY 243 SPRDRPSINSILKRPFLNLPKYLTPTEVIOEFSHMLIC----- 282
Db 245 RPEERPSVRSILRQPIYKQISFFLEATKIKTNKNKNGDSQSKPPFATVVSGEAESNHE 304
QY 269 ----PEVIOEFSHMLICRAG-----APASRHAGKVQK----- 298
Db 305 VIHQPPLSSEGQTYIMGEGKLSQEKPRASGLKSPASLKAHTCKQDLSNTTELATISS 364
QY 299 ----CKIQKV-----RFRGKCPPRS 315
Db 365 VNIDILPAKGRDSVSDGFVQENQPRYLDASNELGICISQVEEEMLDQNTKSSAQPNL 424
QY 316 ISVPIKRNAIL--HENE-----WRPPAGAKARSIMKIERPK----- 350
Db 425 I--PMWSSDIVTGEKNFVKPLQPLIEKQKPKDQSLSPKLECSGTTLAHNSLRLGSS 482
QY 351 -----TAAVCGHYDYVAAQDMLARRAHAKPSYHP--IPQENTGVEDYQETRHGP 398
K-CPPRSRISVPIKRNAILHRNWRPPAGAKARSIMKIE--RPKIAAVCGHYDYVAAQ 365

Db 358 ESCATISINIDIL-----PAERDSANAGVQESQPHVDAADEVD---SQC 402
QY 366 DMLRRRAH-----KPSYHP--IPQENT-GVEDYQETRHGSPSQWPAEYLORKFAQQ 416
Db 403 SISQEKRLQNTKSSDQFGNLLPFRSDGSGDGGSELVKPLYPFN-----KQKPPDDQ 457
QY 417 YKLKVEKQGLRP-----SSAEPNYN-----ORQELRSNGEPRFOELPFR 457
Db 458 VTGIIENODSIHPSRQPHSSNSSELSRQRQKKEQTAHSGTSQFQELPPR 510
RESULT 3
I78885
serine/threonine-specific protein kinase (EC 2.7.1.1-) STK2 - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: I78885
R:Bevedakou, E.N.; He, M.; Baptist, E.W.; Craven, R.J.; Cance, W.G.; Welcsh, P.L.; Simmor
Oncogene 9, 1977-1988, 1994
A:Title: Two novel human serine/threonine kinases with homologies to the cell cycle regul
A:Reference number: I58396; MUID:94268838; PMID:8208544
A:Accession: I78885
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-841 <RES>
A:Cross-references: UNIPROT:P51957; GB:L20321; NID:G348244; PID:AAA36658.1; PID:G348245
C:Genetics:
A:Gene: GDB:STK2
A:Cross-references: GDB:374125
A:Map position: 3p21.1-3p21.1
C:Superfamily: human serine/threonine-specific protein kinase STK2; protein kinase homol
C:Keywords: phosphotransferase
F:4-261/Domain: protein kinase homology <XIN>
Query Match 19.2%; Score 655; DB 1; Length 841;
Best Local Similarity 24.0%; Pred. No. 7e-19;
Matches 195; Conservative 136; Mismatches 251; Indels 230; Gaps 22;
QY 4 YDVVKAIGGAFGKAYLAKGSDSKHCVIKTEINFEKMPIOKEASKKEVILLKMKHPNI 63
Db 6 YCYLRVWVGSGYGEVTLVKHRDQKQYVVKLNLRNASSRRRAAEQAQLLSQKHPNI 65
QY 64 VAFNFSFO-ENGRLFIYMEYCDGDLMKRINRQGVLFSEDIQLGFWFVQISLGLKHIHDR 122
Db 66 VTYKESWEGDGLLYVMGFCEGGDLVYKLEQKQQLLPENQVVEFWQIAVALQYLHEK 125
QY 123 KILHRDIAQNIIFLSKNGWAKLGDGFIARVLNNSMELARTCIGTPYVLSPEICONKPNY 182
Db 126 HILHRDLTKQNVFLRTNII-KVGDGLIARVLEHNDMASTLIGTPYVMSPELFSNKPYN 184
QY 183 NKTIDWSLGCVLVELCTLKHDPFEGNNLQQLVLCQAHFAPISPGFSRELHSLISQLFQV 242
Db 185 YKSDVWALGCCVYEWATLKHAFNAKMNSLVYRIIEGKLPMKPVYVSTELAEILRTLSK 244
QY 243 SPRDRPSINSILKRPFLNLPKYLTPTEVIOEFSHMLIC----- 268
Db 245 RPEERPSVRSILRQPIYKQISFFLEATKIKTNKNKNGDSQSKPPFATVVSGEAESNHE 304
QY 269 ----PEVIOEFSHMLICRAG-----APASRHAGKVQK----- 298
Db 305 VIHQPPLSSEGQTYIMGEGKLSQEKPRASGLKSPASLKAHTCKQDLSNTTELATISS 364
QY 299 ----CKIQKV-----RFRGKCPPRS 315
Db 365 VNIDILPAKGRDSVSDGFVQENQPRYLDASNELGICISQVEEEMLDQNTKSSAQPNL 424
QY 316 ISVPIKRNAIL--HENE-----WRPPAGAKARSIMKIERPK----- 350
Db 425 I--PMWSSDIVTGEKNFVKPLQPLIEKQKPKDQSLSPKLECSGTTLAHNSLRLGSS 482
QY 351 -----TAAVCGHYDYVAAQDMLARRAHAKPSYHP--IPQENTGVEDYQETRHGP 398

RESULT 5
G01452
NIMA-like protein kinase 1 - human
C:Species: Homo sapiens (man)

RESULT 6
T11854

C;Species: Trypanosoma brucei
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Aug-2004
C;Accession: T11854

Mol. Biochem. Parasitol. 59, 111-122, 1993

A;Reference number: Z17363; MUID:93295429; PMID:8515773
A;Accession: T11854

A; Molecule type: mRNA

A; Cross-references: UNI
C; Genetics.

C;Superfamily: protein

QY 216 ICQAHFAPISPGFSRELHSLISOLFQVSPDRDRPSINSILKRPFLNLIPIKYLTPEVIOEE 275
Db 238 ICCGNLSCWDHSDYDFVLLIRHCLVNSDLRTTYTQLLRSPILSDIRSKLESERVVLQ 297
QY 276 FS-----HMLICRAGAPASRHAGKVQCKIQKVRFCGKCPSPRSRISVPIKRNAILHRN 329
Db 298 SLLHKKHQMLQLENDLQFREQLRSASELENV-----IASLA---QREILIRE 347
QY 330 EWPPAGAKARSIKMIERPKIAAVCGHYDYVYQAL--DMLRRRAHKPSYHIPQENTGV 387
Db 348 -----LEK-QLRDMARYQRHMQTVVNSQMKVRVTSPPVDHNEQEPSSFA 390
QY 388 EDYQGETRHPSPSOWPAEVLQKFEAQYKLVKVEQL-----GLRPSASPNYQ--- 438
Db 391 EMFVDTCTEA---SQSPLLHIP-----KLGISPLQTLSCPGTTLTQPIILKRPYL 439
QY 439 QBELRNGEPEPRFQELPFRKNEMKEQEWYKQLEIRQQYLN---DMKEIRKMG--REPE 493
Db 440 RKELSRALHTTATLMKYRAN-----ASSLRTTIDKDGQITSLQKNGT-SNOVA 489
QY 494 DIEKDLKQWRLQNTKESKYPEQ---KYAKKGV-----KFEINLDKCIDENILQEEEA 544
Db 490 DCMNKLHSLDOKKLS--PSELCNKPSPDGEGLPNRKVSKLSVE-----SDETAVSASG 542
QY 545 MDIPNETLTFEDGMKFKYECVKEHGDYTDKAFELHCPPEAAFTLTWLSFLFLEYSLPH 604
Db 543 ESVPTDSTLTDTKSKSVFVHPSPQSLYVEK-LEKLNIRSDVSRKSKATLHGVALPS 601
QY 605 FLEKSPFRRHLIEDLLCANDCSLKDWSEKEMEL 638
Db 602 L---ASPYDVHAEKTIARENE---MDGNFKTMKI 629

RESULT 9
JC7838
Nek6 protein kinase, NIMA histone H3 kinase homolog - human
C:Species: Homo sapiens (man)
C:Date: 09-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 09-Jul-2004
C:Accession: JC7838
R:Hashimoco, Y.; Akita, H.; Hibino, M.; Kohri, K.; Nakanishi, M.
Biochem. Biophys. Res. Commun. 293, 753-758, 2002
A:Title: Identification and characterization of Nek6 protein kinase, a potential human h
A:Reference number: JC7838; MUID:22050088; PMID:12054534
A:Molecule type: mRNA
A:Residues: 1-338 <HAS>
A:Cross-references: UNIPROT:O9HC98; DBJ:AB026289
C:Comment: This protein, a novel member of NIMA (never in mitosis, gene A) related kinas
Playing a conserved central role in regulating mitotic chromosome condensation and asse
C:Genetics:
A:Gene: nek6
A:Map position: 9q33-34

Query Match 13.9%; Score 471.5; DB 2; Length 338;
Best Local Similarity 38.5%; Pred. No. 4.3e-12;
Matches 99; Conservative 53; Mismatches 96; Indels 9; Gaps 6;

QY 4 YDVIIKAGOGAFKAYLAKGSDSKHCVIKEIN-PEKMPIQBKASKKEVILLERKMKHPN 62
Db 70 FOIEKKIGRGQSEVYKATCLLDRTKTVALKVQIPFEMDAKARQDCVKEIGLLKQLNHPN 129
QY 63 IVAFNPSFOENGLFTWMEYCDGDLMKRIN--RQRGVLPSEDDILGMFVQISLGLKHIH 120
Db 130 IIKYLSDFIEDNELNIVLEADAGLSQMIKFKKQRLIPIERTVMKVQVQCSAVEHMH 189
QY 121 DRKILHDIKAOINFLSKNGVAKLGDGFIARVLNNSMELARTCTGTPYLLSPICQNKP 180
Db 190 SRRVMHRDIKPAVNFITAGV- KLGDGLGRFFSSETTAASLSLVGTTPYNSPERIHNG 248
QY 181 YNNKTDIWSLGVLYELCTLKHPFEGN--NLQOLVLIKQAHFAPISPG--FSRELHSLI 236
Db 249 YNFKSDIWSLGLLYEMAALQSPFYGDKNVLFSLQKIEQCQDYPPL-PGEHYSEKRLIV 307

QY 237 SOLFOVSPDRDRPSINSI 253
Db 308 SMCICPDFOHQEPDIGYV 324

RESULT 10
AS7177
NIMA-like protein kinase - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 11-Aug-2003
C:Accession: AS7177
R:Pu, R.T.; Xu, G.; Wu, L.; Vierula, J.; O'Donnell, K.; Ye, X.S.; Osmani, S.A.
J. Biol. Chem. 270, 18110-18116, 1995
A:Title: Isolation of a functional homolog of the cell cycle-specific NIMA protein kinas
A:Reference number: AS7177; MUID:95355415; PMID:7629122
A:Accession: AS7177
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-779 <PUA>
A:Cross-references: GB:L42573; NID:G1040682; PIDN:AAA80145.1; PID:G1040683
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: ATP
F:5-290/Domain: protein kinase homology <KIN>
F:13-21/Region: protein kinase ATP-binding motif

Query Match 13.5%; Score 459; DB 2; Length 779;
Best Local Similarity 25.2%; Pred. No. 2.7e-11;
Matches 160; Conservative 92; Mismatches 194; Indels 190; Gaps 23;

QY 2 DKYDVIIKAGOGAFKAYLAKGSDSKHCVIKEINPEKMPIQBKASKKEVILLERKMKHP 61
Db 5 DKYELLEKIGHGSGFIIRKVRKADGMILCRKEISYLMKSKQEREQLHAEFSILSLRHP 64
QY 62 NIVAFPN--SFOENGLFTWMEYCDGDLMKRI-NRQGVLPSEDDILGM--FVQISLGL 116
Db 65 NIVGYHREHLKATQDLHLYMEYCGDGLGRVIRNLKNNQYAESEFV-WSIFSQLVATL 123
QY 117 KHII-----DRKILHDIKAOINFLSKNGVAKLGDGFI 150
Db 124 YRCHGVDPPEVGKTVLGLGSTARPKPPSGWITLHDLKPEVFLGEDNSV-KLGDGL 182
QY 151 ARVLNNSMELARTCTGTPYLLSPICQNKPNKNTDITWSLGVLYELCTLKHPFEGNQLQ 210
Db 183 SKVM-QSHDFASTYVGTFFYMSPEICAAEYTKLSDIWSLGCIIYELCAREPPFNKATHY 241
QY 211 QVLKICQAHFAPISPGFSRELHSLISOLFQVSPDRDRPSINSILKRPFLNLIPIKYLTPE 270
Db 242 QLVQKIKEGKIAPLPVSYSGELFATIKDCLRVNPDPRDPTATLNLTP-----IVRLMRKE 296
QY 271 VIOBEFSHMLICRAGAPASRHAGKVQCKIQKVRFCGKCPSPRSRISVPIKRNAILHRNE 330
Db 297 KEVVEFSRTL-----RTKEETLNK-RIRELDSKLSALETEKSSIRAEIDASL-RRE 345
QY 331 WRPPAGAKARSIKMIERPKIAAVCGHYDYVYQALDMLRRRAHKPSYHIPQENTGVEDY 390
Db 346 WE-----VKAR-----EIDRL-----VAQE----- 361
QY 391 QGETRHGSPSQWPAEYLQKFEAQYKLVKVEQL---GLRP-----SSA 432
Db 362 -----IESLQOKFE-QEVOARVEAELORHGRGPMFNSHGQOQSFSSTAATL 406
QY 433 EPNTNQRELRSNGEERPFQELPFRKNEMKEQEWYKQLEIRQQYLNLMKEIRKMKR-- 490
Db 407 VSDYNLSVSGDGFPTTDD-----ITDISIAESTDGDITKIPRTPT 450
QY 491 -----EPEDIEK-----DLKQWRLQNTK-ESKNPEQKYKAKK 521
Db 451 FHRAQTYSSAPAESVLGTPMWDIEMASPSPIIASLSLSPERMALTKAPTINPRIF- 506
QY 522 GVKFEINLDKCIDENILQEEHAMDIPNLTLPEDG 557
Db 507 -----GSEPTSTDKNSKNVPRETEMIDSG 530

RESULT 11

T49136
protein kinase-like protein - Arabidopsis thaliana
N:Alternate names: protein F26G5.150
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: T49136
R:D'Angelo, M.; Verzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.; et al.
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25017
A:Accession: T49136
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-941 <DAN>
A:Cross-references: UNIPROT:Q9LXP3; EMBL:AL353814; GSPDB:GN00061; ATSP:F26G5.150
A:Experimental source: cultivar Columbia; BAC clone F26G5
C:Genetics:
A:Gene: ATSP:F26G5.150
A:Map position: 3
A:Introns: 33/2; 55/3; 77/3; 93/2; 108/3; 135/3; 150/1; 166/3; 194/1; 210/3; 218/3; 237/3

Query Match 13.2%; Score 451; DB 2; Length 941;
Best Local Similarity 23.9%; Pred. No. 6.4e-11;
Matches 152; Conservative 117; Mismatches 22; Indels 144; Gaps 22;
QY 1 MDKYDVIKAIQGGAFGKAYLAKGSDSKHCVKEINFEKMPIQEKASKKEVILLERKMK 60
DB 5 MDQYELMEQIGGAFGAAILVHKAERKKYVKKIRLARQTERCRRSAHQMSLIARVQH 64
QY 61 PNIIVAFNSFOENG-RULFIWVEYCDGDLMKRINRQGVLFSEDOILGFWVQISLGLKHI 119
DB 65 PYIVFEKAEWKEQCYCIVTGYCEGGDMALMKNSGVFPPEKCKWFTQLLLAVEYL 124
QY 120 HDRKILHRDIKAQIFISKNGWAKLDFGIARVLNNSMELARTCIPTPYLSPEIQCNK 179
DB 125 HSNVYLHRDLKSNIFLTKDDQV-RLGDFGLAKTL-KADDLTSSWGTPTNMPCELLADI 182
QY 180 PYNKNTDWSLGCVLVELCTLKHPEGNLQOLVLKICQAHFAPISPGFSRELUHLSIQL 239
DB 183 PYGFKSDIWSLGCCLYEMAAVYPAFAKDFMAGLISK-----KSTH----- 222
QY 240 FOVSPDRPSINS-----ILKRPFLNLIPIKY-----LTPE----- 270
DB 223 -QGVNKEPRVSAKMASEILKHPYLQYVQYRPTLSAASITPEKPLNSREGSRMAES 281
QY 271 -----VIQEEFSHMLICRAGAPASR-----HAGVYVQCKIQKVR 305
DB 282 QNSNSSSEKDNFYVSDKNIRYVWPVPSNGNKVTETDSGFVDDDEDILDHVQQAENGILQSV- 340
QY 306 FRGKCPPEPSRISVPKRNAILHRNEWP-----PAGAQAQBSIKMIERPKIAAVCGHYDY 361
DB 341 -SATKPDGHGLIKV-----HSDQRPDVLPQHPKTIINIMVLKEEKARENG----- 387
QY 362 YAOQLMLRRRAHKPSYHIPQENTGVDEYQGETRHGSPSQWP-----ABYLQRKFEAQ 416
DB 388 ----SPNRSNRSRPS--SVPTQKNVE-----TPSKIPLGDIHSSKTNASTPI 431
QY 417 YKLKVEKOLGLRPSAENYNNQRELNSGEPRFQEL---PPKNEKQEYWKQLE-- 471
DB 432 PPSKLADSAARTPGFPFKHPMVIDSPKLPKPNDRISPSPAKHEAEAMSVKRRQRT 491
QY 472 -----BTRQ--QYLDNM--KEIRKKMGREPEDIKDLQMRLQNTKESKNPE 514
DB 492 PPTLPRTSLTAHQSRQLGADISNMAAKETAKLHPSVPSSESNHSQSRVHASPVSVTPE 551
QY 515 QK---YKAKGVKVEINLKDCKISDENILQBEAM 546
DB 552 PKRTSVGSAKMQGESS--NSISSLSNQAFELCD 584

RESULT 12

T21075

hypothetical protein F19H6.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21075; T21124
R:McMurray, A.
submitted to the EMBL Data Library, August 1995
A:Reference number: Z19368
A:Accession: T21075
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-294 <WIL>
A:Cross-references: UNIPROT:Q19530; EMBL:Z50873; PIDN:CAA90762.1; GSPDB:GN00028; CESP:F19H6.1
A:Experimental source: clone F19H6
R:McMurray, A.
submitted to the EMBL Data Library, November 1995
A:Reference number: Z19378
A:Accession: T21124
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-294 <W12>
A:Cross-references: EMBL:Z68115; PIDN:CAA92169.1; GSPDB:GN00028; CESP:F19H6.1
A:Experimental source: clone F19H6
C:Genetics:
A:Gene: CESP:F19H6.1
A:Map position: X
A:Introns: 55/3; 85/2; 113/3; 150/1; 192/3; 266/2
C:Superfamily: kinase-related transforming protein; protein kinase homology
Query Match 12.5%; Score 424; DB 2; Length 294;
Best Local Similarity 37.1%; Pred. No. 2.7e-10;
Matches 85; Conservative 55; Mismatches 83; Indels 6; Gaps 4;
QY 1 MDKYDVIKAIQGGAFGKAYLAKGSDSKHCVKEINFEKMPIQEKASKKEVILLERKMK 59
DB 20 LELFTIEIKIGKQGFSEVFRACQCTWVDLHVALKKIQVEMVDQKARQCLKEIDLLKQLN 79
QY 60 HNIIVAFNSFOENGRLEFIWVEYCDGDLMKRIN--RORGVLFSDDQLGFWVQISLGLK 117
DB 80 HNVIRYVASFIDNNQNLNIVLEAEGDMSRVKHFKGGRLIPEKTIWKYFVQLARALA 139
QY 118 HTHDKILHRDIKAQIFISKNGWAKLDFGIARVLNNSMELARTCIPTPYLSPEIQCNK 177
DB 140 HNHKRMHRDIKPNVFIITGNIV-KLGDGLGRFFSFKTTAAHSLVGTPTYNMSPERIQ 198
QY 178 NKPNYKNTDWSLGCVLVELCTLKHPPEN--NLQQLVLKICQAHFAP 224
DB 199 ESGYNFKSOLWSTGTCLLIYEMAALQSFFYDGKKNLYSLCKKIENCEYPPPL 247

RESULT 13

S23580
probable protein kinase KIN3 (EC 2.7.1.-) - Yeast (Saccharomyces cerevisiae)
N:Alternate names: probable protein kinase FNS2; probable protein kinase NPK1; protein)
C:Species: Saccharomyces cerevisiae
C>Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 16-Aug-2004
C:Accession: S23580; S20123; S40906; S43451; S11185
R:Schweitzer, B.; Philippsen, P.
Mol. Gen. Genet. 234, 164-167, 1992
A:Title: NPK1, a nonessential protein kinase gene in Saccharomyces cerevisiae with similar
A:Reference number: S23580; MUID:92357012; PMID:1495480
A:Accession: S23580
A:Molecule type: DNA
A:Residues: 1-435 <SCH>
A:Cross-references: UNIPROT:P22209; EMBL:X60549; NID:G298024; PIDN:CAA43042.1; PID:G29802;
R:Davies, C.J.; Hurchison III, C.A.
submitted to the EMBL Data Library, January 1992
A:Description: A directed DNA sequencing strategy based upon Tn3 transposon mutagenesis:
A:Reference number: S20123
A:Accession: S20123
A:Molecule type: DNA
A:Residues: 1-435 <DAV>
A:Cross-references: EMBL:M67445
R:Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Fortin, N.; Zeng, B.; Delaney, S.; Oue,

submitted to the EMBL Data Library, November 1993

A:Description: Sequencing of chromosome I of Saccharomyces cerevisiae: Analysis of the 42 kbp
A:Reference number: S40891
A:Accession: S40906
A:Molecule type: DNA
A:Residues: 1-430 <CLA>
A:Cross-references: EMBL:L22015; MIPS:YAR018c
R:Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Fortin, N.; Zeng, B.; Delaney, S.; Oude
Yeast 10, 335-541, 1994
A:Title: Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of the 42 kbp
A:Reference number: S43441; MUID:95028152; PMID:7941740
A:Accession: S4351
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-435 <CLW>
A:Cross-references: EMBL:L22015; NID:g1339990; PIDN:AAC04964.1; PID:G349756
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993
R:Jones, D.G.L.; Rosamond, J.
Gene 90, 87-92, 1990
A:Title: Isolation of a novel protein kinase-encoding gene from yeast by oligodeoxynucleotide
A:Reference number: S11185; MUID:90337351; PMID:2199332
A:Accession: S11185
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-97, 'L', '99-120', 'Q', '122-129', 'I', '131-234', 'SQIS', '239-357', 'R', '359-369 <JON>
A:Cross-references: EMBL:MS5416
A:Experimental source: strain SB303
C:Genetics:
A:Gene: SGD:KIN3; NPK1; FUN52
A:Cross-references: SGD:S0000071; MIPS:YAR018c
A:Map position: IR
C:Superfamily: protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:23-343/Domain: protein kinase homology <KIN>
F:31-39/Region: protein kinase ATP-binding motif

Query Match 12.4%; Score 423; DB 2; Length 435;
Best Local Similarity 27.4%; Pred. No. 4.1e-10;
Matches 123; Conservative 69; Mismatches 141; Indels 116; Gaps 14;

Qy 3 KYDVKAIGGAGTGKAYLAKGSDSKHCYVKEINFEKMPIQEAKSKVILLKMKHPN 62
Db 24 EYQVLEIGKSGSGVGRKVTIHTPTKLLVLRKDIKYGHMNSKRQQLIAECISLSLKHEN 83
Qy 63 IVAFNN-SFOENGR-LPIVMYEDGGDLMKRIN--RQRGLFSEDQILGFVQISLGLKH 118
Db 84 IVEFYNWDFDEQEVLYLYMEYCSRGDLSQWIKHYKQEHKYIPEKIWGLAQLLTALYK 143
Qy 119 IH-----DRK-----ILHRDIKAQNIPLS----- 137
Db 144 CHYGVELPTTITYDRMKPKPVKGNIVIHRLDPGNIFLSYDDSDYNINEQVDGHEVNS 203
Qy 138 -----KNG-----MWAKLGDGFGIAVLNNSMELARTCIGTPYLSPEICQNK 179
Db 204 NYVRDHEVNSGKSGSPMDYSQVVVVLGDFGLAKSLETSIOFATYYGTFPYMSPFVLMQ 263
Qy 180 PYNKNTDWSLGVCLVYELCTLKHFPFEGNNLQQLVKICQAHFAPISGPGFSRELHSLISQL 239
Db 264 PYSPLSDWSLGVCFEPMCSLHPFPQAKNYLELQTKIKNGKCDTPVEYISRGLENAIHSM 323
Qy 240 FQVSPDRPDSINSLTKRPFLENLIPKYLTEVTEQEFESHMLICRAGAPASRHAKVV--- 296
Db 324 IDVNLRTFPS-----TFELQD--IQIRTKSLQLERFERFKULDYE 363
Qy 297 -QKCKIQKVRFRGKCPPRSRISVPIKRNALLHNEWR-----PPAGAKARSIKMIERP 349
Db 364 NELTNIEKI-----LEKQALEYERELSQLKEQFTQAVEERAREV--ISGK 406
Qy 350 KIAVCGHYDYVYQALDMLRRRAHKPSYH 378
Db 407 KVGKVPESINGYVG-----KTFAPKPAYH 429

RESULT 14

B96587
hypothetical protein F20D21.33 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2000 #text_change 09-Jul-2004
C:Accession: B96587
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 409, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B96587
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-200 <STO>
A:Cross-references: UNIPROT:Q9SLI2; GB:AE005173; NID:94585993; PIDN:AAD25629.1; GSPDB:GN
C/Genetics:
A:Gene: F20D21.33
A:Map position: 1

Query Match 12.2%; Score 415.5; DB 2; Length 200;
Best Local Similarity 40.5%; Pred. No. 4.1e-10;
Matches 79; Conservative 51; Mismatches 62; Indels 3; Gaps 3;

Qy 1 MDYDVIKATGAGFGKAVLAKGSDSKHCIVKEINFEKMPIQEKASKKEVILLKMKH 60
Db 1 MEQYEFLEQIGKGSFGSALLVRHKEKKYVLKRIARQTQRTRESAHCVEGLSKMRH 60
Qy 61 PNIVAFNSFOENG-RLFIVMEYCDGDLMKRINRORGVLFSDDQLGHFVQISLGLKHI 119
Db 61 PFIVEXKDSWEXACVYCVIGVCEGDNAQAKKSGNVHFQBEKLCRWLVQLMGLEYL 120
Qy 120 HDRKILHRDIKAQNIFLSKNGMWAKLGDFGIARVLNNSMELARTCTGTPVYLSPEICQNK 179
Db 121 HSNHILHRDVKCSNIFLTKEQDI-RLGDTGLAKIL-TSDDLTSSVVGTFSYMCPELLADI 178
Qy 180 PYNKKTDIWSLGCVL 194
Db 179 PYGSKSDIWSLGTFL 193

RESULT 15

T47988
serine/threonine-protein kinase-like protein - Arabidopsis thaliana
N/Alternate names: protein F21F14.130
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47988
R/Choisne, N.; Robert, C.; Brottler, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, February 2000
A:Reference number: Z24481
A:Accession: T47988
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-648 <CHO>
A:Cross-references: UNIPROT:Q9M269; EMBL:AL138642
A:Experimental source: cultivar Columbia; EAC clone F21F14
C/Genetics:
A:Map position: 3
A:Introns: 77/3; 117/1; 136/3; 158/2; 189/3; 216/3; 254/1; 272/2; 483/3; 563/1; 586/3
A:Note: F21F14.130

Query Match 12.0%; Score 410; DB 2; Length 648;
Best Local Similarity 34.2%; Pred. No. 1.8e-09;
Matches 94; Conservative 56; Mismatches 111; Indels 14; Gaps 7;

Qy 10 IGGAGFGKAVLAKGSDSKHCIVKEINFEKMPIQEKASKKEVILLKMKHFNIVAFNS 69

GenCore version 5.1.6
Copyright (C) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2004, 12:45:34 ; Search time 198 Seconds

(without alignments)
1859.737 Million cell updates/sec

Title: US-10-730-010-2

Perfect score: 3404

Sequence: 1 MDKYDIKAIQGAGFKAYL.....LCANDCSLKDWSEKEMELRT 640

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% --

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3069	90.2	708	2	Q6P3R8	Q6P3R8 homo sapien
2	3069	90.2	708	2	AAH33885	Aah33885 homo sapi
3	1840.5	48.2	614	2	Q8CCJ0	Q8CCJ0 mus musculus
4	1640.5	48.2	627	2	Q7TSC3	Q7TSC3 mus musculus
5	1135.5	33.4	336	2	Q8CGN6	Q8CGN6 mus musculus
6	1078	31.7	774	1	NEK1_MOUSE	P51954 mus musculus
7	1042	30.6	1258	1	NEK1_HUMAN	Q96PY6 homo sapien
8	1004.5	29.5	424	2	Q8CD72	Q8CD72 mus musculus
9	966	28.4	302	2	Q8S5B6	Q8S5B6 mus musculus
10	850	25.0	898	2	Q7QQZ8	Q7QQZ8 giardia lam
11	810.5	23.8	506	1	NEK3_HUMAN	P51956 homo sapien
12	805.5	23.7	511	1	NEK3_MOUSE	Q9R0A5 mus musculus
13	802.5	23.6	509	2	Q99K72	Q99K72 mus musculus
14	802	23.6	510	2	Q6ZN64	Q6ZN64 homo sapien
15	802	23.6	510	2	BAD18511	BAD18511 homo sapi
16	799	23.5	489	2	Q8U023	Q8U023 homo sapien
17	757	22.2	492	2	Q6INC0	Q6INC0 xenopus lae
18	757	22.2	492	2	AAH72363	Aah72363 xenopus l
19	741	21.8	494	2	Q6DUQ5	Q6DUQ5 xenopus tro
20	675.5	19.8	1123	2	Q6E106	Q6E106 dictyosteli
21	675	19.8	781	2	Q6P576	Q6P576 homo sapien
22	675	19.8	781	2	AAH53044	Aah53044 homo sapi
23	675	19.8	849	2	Q7T299	Q7T299 brachydanio
24	668.5	19.6	790	2	Q6NU24	Q6NU24 xenopus lae
25	668.5	19.6	790	2	AAH68778	Aah68778 xenopus l
26	664.5	19.5	911	2	Q6UPR3	Q6UPR3 chlamydomon
27	664.5	19.5	911	2	AAQ64684	Aaq64684 chlamydom
28	659.5	19.4	792	1	NEK4_MOUSE	Q9ZJ12 mus musculus
29	655	19.2	841	1	NEK4_HUMAN	P51957 homo sapien
30	651.5	19.1	792	2	AAH57939	Aah57939 mus muscu
31	638	18.7	692	1	NEK8_HUMAN	Q86896 homo sapien

32 638 18.7 697 2 Q6DJA8 Q6dja8 xenopus tro
33 634 18.6 698 1 NEK8_MOUSE Q91Zr4 mus musculu
34 634 18.6 698 2 AAH70457 Aah70457 mus muscu
35 624 18.3 555 2 Q9N9C3 Q9n9c3 leishmania
36 623 18.3 697 1 NEK8_BRARE Q90xc2 brachydanio
37 622 18.3 812 2 Q6UPR1 Q6upr1 chlamydomon
38 622 18.3 812 2 AAQ64686 Aaq64686 chlamydom
39 590 17.3 645 2 Q8NG66 Q8ng66 homo sapien
40 588.5 17.3 637 2 Q8WNU8 Q8wnu8 macaca fasc
41 586.5 17.2 628 2 Q8C0Q4 Q8c0q4 mus musculu
42 584 17.2 482 2 Q8TBY1 Q8tby1 homo sapien
43 582.5 17.1 470 2 Q8NG65 Q8ng65 homo sapien
44 575 16.9 579 2 Q95XQ3 Q95xq3 caenorhabdi
45 571 16.8 365 2 Q8BW62 Q8bw62 mus musculu

ALIGNMENTS

RESULT 1
Q6P3R8
ID Q6P3R8 PRELIMINARY; PRT; 708 AA.
AC Q6P3R8;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE MGC75495 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Haie S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski N.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC063885; AAH63885.1; -
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase..
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.

RESULT 3

Q8CCU0 PRELIMINARY; PRT; 614 AA.

AC Q8CCU0;

DT 01-MAR-2003 (T-EMBLrel. 23, Created)

DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)

DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)

DE Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length

DE enriched library, clone:653041J22 product:weakly similar to protein

DE kinase nek1 (EC 2.7.1.-).

GN Name=BB049667;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_taxid=10090;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RX MEDLINE=99279253; PubMed=10349636;

RA Carninci P., Havaashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44 (1999).

[2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RX MEDLINE=21085660; PubMed=11217851;

RA RIKEN FANTOM Consortium;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690 (2001).

[3]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RA The FANTOM Consortium;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573 (2002).

[4]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RX MEDLINE=20439374; PubMed=11042159;

RA Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to

RT prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Genome Res. 10:1617-1630 (2000).

[5]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RX MEDLINE=20530913; PubMed=11076861;

RA Shibata K., Itoh M., Aizawa K., Hamagaki T., Hara A., Hashizume W.,

RA Konno H., Akiyama J., Nishi K., Katsuna M., Nishine T., Harada A.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsueura S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format

RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771 (2000).

[6]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kawaga I., Kasukawa T.,

RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Kurihara C., Matsuyama I., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

Db 461 NRQW-----DAGAPHTLL 474

RESULT 4

Q7TSC3 PRELIMINARY; PRT; 627 AA.

AC Q7TSC3; (TREMELrel. 25, Created)

DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)

DT 01-VAR-2004 (TREMELrel. 26, Last annotation update)

DE BB049667 protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

OX NCBI_TaxID=10090;

RN [1]_

RP SEQUENCE FROM N.A.

RC TISSUE=Olfactory epithelium;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,

RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley D.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Olfactory epithelium;

RA Strausberg R.;

EL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

DR EMBL; BC053516; AAH53516.1; -.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR000719; Prot.kinase.

DR InterPro; IPR002290; Ser_thr_kinase.

DR InterPro; IPR008271; Ser_thr_kin_AS.

DR Pfam; PF00069; Pkinase; 1.

DR ProDom; PD000001; Prot.kinase; 1.

DR SMART; SM00220; S_TKc; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.

DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SQ SEQUENCE 627 AA; 71790 MW; AD579B96621ACA2F CRC64;

Query Match 48.2%; Score 1640.5; DB 2; Length 627;

Best Local Similarity 54.8%; Pred. No. 5.8e-82;

Matches 340; Conservative 49; Mismatches 72; Indels 159; Gaps 9;

QY 1 MDKYDVTKAICGAGFKAYLAGKSDSKHCVIKENFERKMPIDQEKASKKEVILLERQKH 60

Db 1 MDNFKLIKIGEGTFGKVKYLAKDSKSSSHCVIKESLTK---EKEASKNEVILLARMEH 56

QY 61 PNIVAFNSFQENGRLFVMEYCDGGDLMKRINQRGVLFPSDQILGWVQISGLKHH 120

Db 57 PNIVTFSSFQENGRLFVMEYCDGGDLMQRIQRQGVWFSDDQILGWVQISGLKHH 116

QY 121 DRKILHDIKAONIPLSKNGVAKLGDGFIARVLNNSMELARTCTGTPYLSPEICQNP 180

Db 117 DRKILHDIKSONIFLSKNGVAKLGDGFIATNTLNSMELAQCTAGTTPYLSPEICQNP 176

QY 181 YNNKTDINSLGCVLYELCTLKHPPFEGNNLQQLVWKICQAHFAPISPGFSRELHSLISOLF 240

Db 177 YNNKTDINSLGCVLYELCTLKHPPFESSNNFHLVLKICQGRVAPISPHFSRDLQSLPOLF 236

QY 241 QVSPDRPSINSILKRPFLNLIPLYTPVIOEBSFSEHMLCRAGAPASRAGKVVQCK 300

Db 237 RVSPQDRPSVTLKRPFLNLIPLYTPVIOEBSFSEHMLCRAGAPASRAGKVVQCK 267

QY 301 IQKVRPRGKCPRRISVPIKRNAILHRNWRPPAGAKARSIKMIERFKIAAVCGHYD 360

Db 268 -----CSR----- 271

QY 361 YVAQLDMLRRRAHKPSYHPIPOENTGVEDYGOETHRGSP-----SQPAEYLQRKFAQQ 416

Db 272 -----IQSHAH-----MENVAI-----GPTACWRVSPWSAAYLQRKFAQQ 307

QY 417 YKLKVEKQLGLRPSAEPNYNORQLRNSGEBEPFOELPFRKNEMKEQBYWKQLEIRQQ 476

Db 308 YKLKVERQLGLRPSVVEHPNVEKELQSHWETKEFQELQYRKNKQDQBYWKQLEIRQQ 367

QY 477 YLNDKKEIRKQGRPEPEDIKDLQKWLQNTKESKNPEQKYAKKGVFEINLQKISDE 536

Db 368 YHNDKKEIKKMGRE-----LKRVRKFEISLQKISDE 400

QY 537 NILQSEAMDIENETLTEDGKFKYECVKEHGDTDKAREKLHCP-----AAF 587

Db 401 DTVQNEAVDKLNATLSPEDGKFGQHRCKBEHEDYDRAFEELCGPRAEGFFQDVIAAE 460

QY 588 TELTWLSFLFLYSLPFL 607

Db 461 NRQW-----DAGAPHTLL 474

RESULT 5

Q8C6N6 PRELIMINARY; PRT; 336 AA.

ID Q8C6N6;

AC Q8C6N6;

DT 01-VAR-2003 (TREMELrel. 23, Created)

DT 01-VAR-2004 (TREMELrel. 26, Last annotation update)

DE Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN full-length enriched library, clone:E2300241i2 product:weakly similar to protein kinase nek1 (EC 2.7.1.-).

DE Name=BB049667;

GN Mus musculus (Mouse).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Oviduct;

RX MEDLINE=99279253; PubMed=10349636;

RA Carninci P., Hayashizaki Y.,

RA "High-efficiency full-length cDNA cloning."

RL Meth. Enzymol. 303:19-44 (1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Oviduct;

RX MEDLINE=21085660; PubMed=11217851;

RA RIKEN FANTOM Consortium;

RT "Functional annotation of a full-length mouse cDNA collection."

RL Nature 409:685-690 (2001).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Oviduct;

RA The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of


```

RT 60,770 full-length cDNAs." ;
RL Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes." ;
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Katsunai T., Tashiro H., Itoh M.,
RA Konno H., Akiyama J., Nishi K., Kitsumai T., Nishine T., Harada A.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Ikegami T., Kashiwagi K.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ogawa Y., Izawa M., Ohara E., Watahiki M.,
RA Fujiwaka S., Inoue K., Togawa Y., Tanaka T., Matsuura S., Kawai J.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer." ;
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Haehizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa T., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Nomazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya I., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBS databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AK054168; BAC35677.1; -.
DR HSSP; P31751; 1GZK.
DR MGD; MGI:2142824; B049667.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR007119; Prot_kinase.
DR InterPro; IPR002230; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc_1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 336 AA; 38757 MW; 6BDD377D72E0143B CRC64;

Query Match 33.4%; Score 1135.5; DB 2; Length 336;
Best Local Similarity 77.0%; Pred. No. 1.4e-54;
Matches 217; Conservative 22; Mismatches 36; Indels 7; Gaps 2;

QY 1 MDKDYIVKAGGAFGAYLAKGSDSKHCVCVKEINFEKMPQKEASKEVILLERKMH 60
Db 1 MDNFKLKIIGSTGKVLAKDKSESHCVIKEISLTK-----EKEASKEVILLARMEH 56
QY 61 PHIVAFNSFQNGRLFIWVEYCDGDLMKRINRQGVLFSEDIQLGWFWQISLGLKHH 120

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Db 57 PNIVTFSSFGNGRLFIWVEYCDGDLMKRIFQRCQGMFSEDIQLGWFWQISLGLKHH 116
QY 121 DRKILHRDIKAQNIPLSKNGWVAKLGDGFIARVNNNSMELARICITGTPYLSPEICNKP 180
Db 117 DRKILHRDIKSONIFLSKNGWVAKLGDGFTARTINDSMELAQTCAGTFYLSPEICNRP 176
QY 181 YNNKTDIWSLGCVLVLYELCTLKHPPEGNLQOLVLIKQAHFAPISPGFSFELHSLISOLF 240
Db 177 YNNKTDIWSLGCVLVLYELCTLKHPFESNNFHLVLIKQGRVAPISPHFSFDLSLISOLF 236
QY 241 QVSPDRPSINSILKRPFLNLIPLKYLTPEVIQ---EEFSHM 279
Db 237 RVSPQDRPSVTSLLKRPFLNLIPLKYLTPEVIQ---EEFSHM 278

RESULT 6
NEKI_MOUSE
ID NEKI_MOUSE STANDARD; PRT; 774 AA.
AC P51954;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase Nek1 (EC 2.7.1.37) (NIMA-related
DE protein kinase 1).
GN Name=Neki;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93010942; PubMed=1382974;
RA Letwin K., Mizzen L., Motro B., Ben-David Y., Bernstein A., Pawson T.;
RT "A mammalian dual specificity protein kinase, Nek1, is related to the
RT NIMA cell cycle regulator and highly expressed in meiotic germ
RT cells." ;
RL EMBL J. 11:3521-3531 (1992).
CC -!- FUNCTION: Phosphorylates serines and threonines, but also appears
CC to possess tyrosine kinase activity. Implicated in the control of
CC meiosis.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- TISSUE SPECIFICITY: Predominantly in testes (germ cells and
CC sertoli cells). Lower levels in ovary (ovocytes and granulosa
CC cells), thymus and lung.
CC -!- DEVELOPMENTAL STAGE: In female, expressed as follicles enter the
CC secondary stage until ovulation occurs. In the male reproductive
CC system, the expression is limited to spermatocytes and spermatids.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. NIMA
CC subfamily.
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DR EMBL; S45828; AAB23529.1; -.
DR PIR; S25284; S25284.
DR HSSP; Q13153; 1F3M.
DR MGD; MGI:97303; Nek1.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.

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DR ProDom; P0000001; Prot kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 898 AA; 102288 MW; C4871A12317ED638 CRC64;

Query Match 25.0%; Score 850; DB 2; Length 898;
 Best Local Similarity 32.4%; Pred. No.1.9e-38;
 Matches 214; Conservative 97; Mismatches 156; Indels 154; Gaps 17;

Qy	1	MDKYDVITKATGCGAFGKAYLAKGSDSKSCHVIVKEINFEKMPIQKEASKVEVILLKKKH	60
Dd	1	MERYKELKLVKGSGFSAVLAQEKSTGIKVMKVHIAPLKPREREALTEAKLSLKKH	60
Qy	61	PNIVAFNSFQENGRLEPIVMVEYCDGGDLMKRINRQ--RGVLFSDQDLGLHFVQISLGLKH	118
Dd	61	PIYVGYHESPADTRYLHVVEYADAGDLTDAIKRQKMKNSLFFEDQLWDFVQICMAKHX	120
Qy	119	IHDRKILHRDIKAQNIPL-----SKMGWAKLGDGFIARVNNMSMELARTCIGTPYVLSLP	173
Dd	121	VHDRKILHRDLKQNIPLCTDENDRSKRTVKLGDGFIAGIKLQSTLECAITAIGTPYVLSLP	180
Qy	174	EICONKPYNNKTDIWSLGGCVLYELCTLKHFPFEGNNLQOLVKLICOAHFAPISPGFSRELH	233
Dd	181	ELCEDKPYNNKSDIWSLGGCVLYELCTLQHAFAEQNMKGLVVKILRGQYQIPISNTYSNLR	240
Qy	234	SLISQLFQVSPRRPSSINSILKRPFLLENLIPKYLTPETVIOEBSHMLICRAG-----	285
Dd	241	EVLDRMLQDKPNKRPSSYNQLKLPLFLQERIRRLLPEDYWNNEEFSHTTIHGRGNALVGFGA	300
Qy	286	-----APASRHAGKVVQCKTIQKVRFGKGCPPSRIS	317
Dd	301	GRVGIPOKPSVGPVKDDASSEASSAGRPASRHGPPSAH-----PPPPSPQQN	349
Qy	318	VPIKRNAILHRNWRPPAGAQK-----ARSIKMIERPK-----	350
Dd	350	KPMYFNP--NGGYQPPAANKLSAAEVAAMAKNNQRPVPPVQSNVQKPGIMPAGI	406
Qy	351	IAAVCG-----HYDYVYAO-----LDMLRRRAHKP-----SYHPIQP	382
Dd	407	AVGVPGAPPVVQNNKLSYDEIVQEKRIEQRRIYQEDQARAEKVRQDYIKYHAAQQ	466
Qy	383	ENTG-----VEDYGOETR-----HGPSPSQWPA-----EYLQRKFEAQYKLVK	421
Dd	467	ENRGYHAVGNPFAKQAQOASCPAGGHAAPSADMLDAKPADLQDFINRPAQAQPPSPR	526
Qy	422	EKQLGLRPSAENYVQRELNRNGEPPRQELPPRKN-----EMKCEQYKQL-----E	471
Dd	527	QSQ---APSSISQPTKQQQQQQQQQQQQQQQQQQQQQDAIRNTEEQRRHQEQVKROLAPAPLKE	583
Qy	472	EIRQQVLDNMKEIRKMGREPEDIKDLQMR-----LQNTKSKNPEQKYKAKGV	523
Dd	584	QAKDAERELMEAHNVQKQKEEQERRIREAKEKQPAEWEKKNREVEKQWEKKAQAQA	643
Qy	524	K 524	
Dd	644	E 644	

RESULT 11
 NEK3_HUMAN STANDARD; PRT; 506 AA.
 AC P51956; Q8WUN5;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Serine/threonine-protein kinase Nek3 (EC 2.7.1.37) (NimaA-related
 DE protein kinase 3) (HSPK 36).
 GN Homo=NEK3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Rana S.S., Joquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guadagnoli P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.S., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RN SEQUENCE OF 48-506 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94368699; PubMed=7522034;
RA Schultz S.J., Fry A.M., Suetterlin C., Ried T., Nigg E.A.;
RA "Cell cycle-dependent expression of Nek2, a novel human protein kinase
RT related to the NIMA mitotic regulator of Aspergillus nidulans";
RL Cell Growth Differ. 5:625-635 (1994).
RN [3]
RN SEQUENCE OF 76-189 FROM N.A.
RX MEDLINE=94100173; PubMed=8274451;
RA Schultz S.J., Nigg E.A.;
RT "Identification of 21 novel human protein kinases, including 3 members
RT of a family related to the cell cycle regulator nima of Aspergillus
RT nidulans";
RL Cell Growth Differ. 4:821-830 (1993).
CC -!- FUNCTION: Kinase that may play a role in mitotic regulation.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Belongs to the Ser/thr protein kinase family. NIMA
CC subfamily.
CC
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CC
CC EMBL; BC019916; AAH19916.2; -
CC EMBL; Z29067; CAAB2310.1; -
CC EMBL; Z25434; CAAB0921.1; -
CC PIR; I38224; I38224.
CC HSP; P71584; 106Y.
CC Genew; HGNC:7746; NEK3.
CC MIM; 604044; -
CC GO; GO:0005634; C:nucleus; NAS.
CC GO; GO:0005524; F:ATP binding; NAS.
CC GO; GO:0004674; F:protein serine/threonine kinase activity; NAS.
CC GO; GO:0007049; P:cell cycle; NAS.
CC GO; GO:0007067; P:mitosis; NAS.
CC GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
CC InterPro; IPR011009; Kinase-like.
CC InterPro; IPR008719; Prot_Kinase.
CC InterPro; IPR008271; Ser_thr_kin_AS.
CC InterPro; IPR001245; Tyr_kinase.
CC Pfam; PF00069; Pkinase; I.
CC PRINTS; PRC0109; TYRKINASE.

DR ProDom; PDC000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Cell cycle; Cell division; Mitosis; Nuclear protein;
KW Phosphorylation; Serine/threonine-protein kinase; Transferase.
FT DOMAIN 4 257 protein kinase.
FT NP_BIND 10 18 ATP (By similarity).
FT BINDING 33 33 ATP (By similarity).
FT ACT_SITE 127 127 Proton acceptor (By similarity).
FT MOD_RES 161 161 Phosphothreonine (by autocatalysis) (By
FT similarity).
FT CONFLICT 54 54 L -> S (in Ref. 2).
FT CONFLICT 77 78 IV -> LV (in Ref. 3).
FT CONFLICT 187 189 SLG -> PSV (in Ref. 3).
SQ SEQUENCE 506 AA; 57704 MW; 4437EB4A41A4777 CRC64;

Query Match 23.8%; Score 810.5; DB 1; Length 506;
Best Local Similarity 34.2%; Pred. No. 1.5e-36;
Matches 193; Conservative 90; Mismatches 169; Indels 113; Gaps 14;

QY 1 MDKYDVIKAIQCGAFGKAYLAKGSDSKHCYKVIKEINFEKMPLOEKEASKKEVILEKMKH 60
DB 1 MDDYMLVRLMIGEGSFGRLLVQHSSNQMFANKEIRLPK-SFSNTQNSRKEAVLLAKMKH 59

QY 61 PNIVAFNSFQENGRLFIIVMEYCDGDLMKRINRQGVLFSEDIILGMFVQISLGLKHIIH 120
DB 60 PNIVAFKESFEAGHLIIVMEYCDGDLQKIKQKQKGLPDDMLNWFQMCILGVNHHI 119

QY 121 DKILHRDIKQNTPLSKNGVAKLGDGFIARVLNNSMELARTICIGTPYVLSPEICNKP 180
DB 120 KKRVLHRDIKKNIFLTQNGKY-KIGDPSARLLSNPMFACTVYGTVPYVPPPEIWENLP 178

QY 181 YNNKTDIWSLGCVLVELCTLKHPPFEGNNLOQLVKIKCOAHFAPISPGFSRELHSLISQLF 240
DB 179 YNNKSDIWSLGCILVELCTLKHFTQANSKNNLLKVCQGCISPLPSHYVELQFLVKQMF 238

QY 241 QVSPDRDRSINSILKRPFLENLIPKLTPEVIOEFSHMLICRAGAPASRHAGKVQCK 300
DB 239 KKNPSHRPSATLLSRGIVARLVQKLPPEIME-----YGEVLEBEIK 282

QY 301 IQKVFRGCKPSPRSISPIKENAILHNEWRPAGAKARSIMKIERPKIAACVGHYD 360
DB 283 NSKHTNPKKNPSRIRALNEASTVQEEQDKGS----- 319

QY 361 YYAQLDMLRRRAHKPSYHPIQENTGVEDYQGETRHGSPS-----QWPAEYLQRKFEAQ 416
DB 320 -HTDLESINELVESALRRVNRKGG--NKSVHLRKASSPNLHRRQW----- 363

QY 417 YKLKVEKQLGLPSSAEPNYQRELRSN--GEPR-FQELPFRKNEMKEQYKQLBEI 473
DB 364 -----EKNV---PNTALTALENASILTSSLTAEDDGGSGVIKSNTRKQ--W--LKET 411

QY 474 RQVYLDNKE-----IRKKNGRE-----PEDIE 496
DB 412 PDLNLILKNADLSLAFQTYIYRPGSEGLKGPLSETEASDSVDGGHDSVILDPERLE 471

QY 497 KDLKQMLQNTKESKNPEQYKAKK 521
DB 472 PGLDEEDTDPEEDDNDPDWSELKK 496

RESULT 12
NEK3_MOUSE
ID NEK3_MOUSE STANDARD; PRT; 511 AA.
AC Q9ROA5; Q920X9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase Nek3 (EC 2.7.1.37) (Nima-related
DE protein kinase 3).
DE Name=Nek3;
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99240743; PubMed=10224116;
 RX Tanaka K., Nigg E.A.;
 RT "Cloning and characterization of the murine Nek3 protein kinase. a
 RT novel member of the NIMA family of putative cell cycle regulators";
 RL J. Biol. Chem. 274:13491-13497(1999).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99321807; PubMed=10393247;
 RA Chen A., Yanai A., Arama E., Kilfin G., Motro B.;
 RT "NIMA-related kinases: isolation and characterization of murine nek3
 RT and nek4 cDNAs, and chromosomal localization of nek1, nek2 and nek3";
 RL Gene 234:127-137(1999).
 CC
 CC !- FUNCTION: Kinase that may play a role in mitotic regulation.
 CC !- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC !- SIMILARITY: Belongs to the Ser/Thr protein kinase family. NIMA
 CC subfamily.
 CC
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 CC
 CC EMBL; AF093416; RAD20986.1; --
 CC EMBL; AF093066; RAD18286.1; --
 CC HSSP; P31751; IGZK.
 CC MGD; MGI:1344371; Nek3.
 CC InterPro; IPR011009; Kinase like.
 CC InterPro; IPR000719; Prot Kinase.
 CC InterPro; IPR002290; Ser Thr kinase.
 CC InterPro; IPR008271; Ser_thr_kin_AS.
 CC InterPro; IPR001245; Tyr_kinase.
 CC Pfam; PF00669; Pkinase; 1.
 CC PRINTS; P00109; TYRKINASE.
 CC ProDom; PD000001; Prot Kinase.
 CC SMART; SM00220; S_TKc_1.
 CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 CC ATP-binding; Cell cycle; Cell division; Mitosis; Nuclear protein;
 KW Phosphorylation; Serine/threonine-protein kinase; Transferase.
 FT DOMAIN 4 255
 FT NP_BIND 10 18
 FT BINDING 33 33
 FT ACT_SITE 125 125
 FT MOD_RES 159 159
 FT CONFLICT 239 239
 FT CONFLICT 342 343
 FT SEQUENCE 511 AA; 57222 MW; D6D6C0533C7302F CRC64;
 Query Match 23.7%; Score 805.5; DB 1; Length 511;
 Best Local Similarity 34.8%; Pred. No. 2.8e-36;
 Matches 194; Conservative 88; Mismatches 184; Indels 91; Gaps 13;
 QY 1 MDKYDVIKAGDGFAGKAYLAKGKSDKHCVKIKENFEKMPIQEAKSKKEVILEKMKH 60
 DB 1 MDNYTVLRVIGGSGFRALLVLQESSNQTFFAKELRLK---SDTQSRKEAVILAKMKH 57
 QY 61 PNIVAFNFSQNGELFTVMEYCDGDLKMKRINRQGVLFSEDOILGFVQISGLKXIH 120
 DB 58 PNIVAFKESFEAEGLYIWMYCDGDLKMKRINRQGVLFSEDOILGFVQISGLKXIH 117
 QY 121 DKILHRDIKQNIPLSKNGKVAKLDGFIARVLNNSMELARTICIGTPYILSPICQKWP 180
 DB 118 KRVLRDIKSNVFLTNKGV-KUGDFGSARLLSSPMFACTVGTGTPYVPPWENLNP 176

QY 181 YNNTDIWSLGCVLVELCTKHPFEGNNLQOLVLKICQAHFAPISPGFSRELHSLISOLF 240
 DB 177 YNKSDDIWSLGCVLVELCALKHPFQANSWKNLILKICQGPILHLPALYSCKLQGLVKQML 236
 QY 241 QVSPDRPFSINILKRPFLNLPKYLTPVIOEFSHMLICRAGAFASHAGKVVCKCK 300
 DB 237 KENSHPSATILLCRGLAPLPKLPQIIRE-----YGEILDEIK 280
 QY 301 IQKVRFGKCPPRSRISVIPKRNAILHRNWRPAGAKARSIMIERPKIAAVCGHYDY 360
 DB 281 ISTPKNVKK-----QDSNRVGRALGEANSAAQBEER-GRKCSHTE- 320
 QY 361 YYAQLDLRRRAHKPSVHPIPO-----ENTGVEDYQET-----RCPS---P 400
 DB 321 -----LESTGTPAGNALGRAAGNPESGNQEHGSHTSPPASHPRPVWERHGPSSNVE 373
 QY 401 SQWPAEYLQRFKAQYK----LKVEKQLGLRPSAEFPYNNQRELRSNGEERFQELP- 455
 DB 374 ALEKASILTSSFTAEDDRGGSVIKYEN-ARRQWVREPPALLSMLKDALDSQAFQYTI 432
 QY 456 -----FRKNEMKEQYWKQLSEIROQYLNDMKETKMGKREPEDIKDLKQVRLQNTK 508
 DB 433 YRPAEGFLKGPUSEDTASDVGDLDVMDLDPERFELDEDTDFEED----- 482
 QY 509 ESKNPEQKYKAKKGVK 525
 DB 483 -NENPDWVSELKKGVG 498
 RESULT 13
 Q99K72 PRELIMINARY; PRT; 509 AA.
 AC Q99K72;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Nek3 protein.
 GN Name=Nek3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II;
 RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Skalko U., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Kzywinski M.I., Skalko U., Schmutz J., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II;
 RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
 RA Srausberg R.

AC	Q6ZN64;	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DT	05-JUL-2004 (TrEMBLrel. 27, Created)	
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	
DE	Hypothetical protein FLJ16392.	
OS	Homo sapiens (Human)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Trachea;	
RA	Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,	
RA	Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,	
RA	Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A.,	
RA	Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,	
RA	Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,	
RA	Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,	
RA	Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.,	
RA	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.	
RL	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.	
CC	EMBL; AK131359; BAD18511.1; -	
DR	GO: GO:0016301; F:kinase activity; IEA.	
DR	InterPro: IPR011009; Kinase like.	
DR	InterPro: IPR000719; Prot_kinase.	
DR	InterPro: IPR002290; Ser_Thr_pkinase.	
DR	InterPro: IPR008271; Ser_Thr_pkin_AS.	
DR	InterPro: IPR001245; Tyr_pkinase.	
DR	InterPro: IPR00069; Pkinase; I.	
DR	PRINTS; PR00109; TYRKINASE.	
DR	ProDom; PD000001; Prot_kinase; 1.	
DR	SMART; SM00220; S_TKC; 1.	
DR	SMART; SM00219; Tyrc; 1.	
DR	PROSITE; PS00107; PROTEIN KINASE ATP; 1.	
DR	PROSITE; PS00011; PROTEIN KINASE_DOM; 1.	
DR	PROSITE; PS00108; PROTEIN KINASE_ST; 1.	
KW	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.	
SQ	SEQUENCE 509 AA; 57109 MW; 333585D058868A1 CRC64;	
Query Match 23.6%; Score 802.5; DB 2; Length 509;		
Best Local Similarity 34.8%; Pred. No. 4e-36;		
Matches 193; Conservative 89; Mismatches 184; Indels 89; Gaps 13;		
QY	1 MDKYDVIKAIQGGAFKAYLAKGSDSKHCVIKFINKPKPIQEKASKEVILKMKH 60	
DB	1 MDNVTVLRVIGQSGFGRALLVQSSNQTFAMKEIRLLK---SDTQTSKEAVLLAKMKH 57	
QY	61 PNIVAFNSFQNGRLFTVMEYCDGGDLMKRINRQGVLFSEQILGWVQISLGLKHIH 120	
DB	58 PNIVAFKESFEAEGLYIVMEYCDGGDMQRIKQKGLFPEDTLNWFQICLGVNHH 117	
QY	121 DRKLHLDIAKQNIPLSKNGVMKLGDFGIARVLNNSMELARTICIGTPPYLSPEIQNKP 180	
DB	118 KRVLRHDIKSNVFLTHNGKV-KLGDGSGARLLSSPMFACTVGTGYVPPPIEWENLP 176	
QY	181 YNNKTDIWSLGCYLVEICTLKHPPGNNLQOLVKICQAHFAPISPGFSRELHLSLSOLF 240	
DB	177 YNNKSDIWSLGCILYELCALKHPQANSWKNLILKICQGIHPLPALYSCKLQDLVKQML 236	
QY	241 QVSPDRPSINSILKRPFFLENLIPKYLTPVIOEFSHMLICRAGAPASHPAGKVVQCK 300	
DB	237 KRNPSHRPSVTLLCRSLAPLVKCLPPQIIE-----YGEQILDEIK 280	
QY	301 IQKVRFRGKCPPRSIRISVPIKRNAILHRNEWPPAGAKARSIMTERPKIAAVCGHYD 360	
DB	281 ISTPKMKK-----QDSNRVGRALGEANSQMQUEER-GRKCSHTE- 320	
QY	361 YYAQDLMLRRRAHKPSYHPIDQNTG---VEDYQDET-----RHGPS---PSQ 402	
DB	321 -----LESTGTFPAGNALGRAAGNPQNGPQEHGRTSPASHPRWRHSGSSNVLEAL 373	
QY	403 WPAEYLRQKFAQGVK-----LKVEKQLGLRPSSEAPNPNQRELRSNGEPREFQELP--- 455	
DB	374 EKASILSSFTABDDRGSVVKYEN-ARROWVREPPPEALLSMKADLADLSQAFQTVTIYR 432	
QY	456 -----FRNEMKEQYWKQLEIEQQVINDMKIRKQKGRPEPDIEKDLQKMLQNTKES 510	
DB	433 PGAEGLKPLGSEPTASDSDVDGLDSVMDLPERFERPELDEEDTDFESD-----N 481	
QY	511 KNPQKYKAKGVKF 525	
DB	482 ENPDWLSELKKGVG 496	
RESULT 14		
Q6ZN64		
ID	Q6ZN64	
PRT; 510 AA.		
PRELIMINARY;		
BAD18511		
ID	BAD18511	
PRT; 510 AA.		
PRELIMINARY;		
AC BADI8511		
DT	12-MAY-2004 (TrEMBLrel. 27, Created)	
DT	12-MAY-2004 (TrEMBLrel. 27, Last sequence update)	
DT	12-MAY-2004 (TrEMBLrel. 27, Last annotation update)	
DE	CDNA FLJ16392 fis, clone TRACH2020048, moderately similar to Mus musculus serine/threonine-protein kinase NEK3 (Nek3) mRNA.	

Search completed: November 12, 2004, 13:00:20
Job time : 203 secs

Search completed: November 12, 2004, 13:00:20
Job time : 203 secs

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OM protein - protein search, using sw model

Run on: - November 12, 2004, 13:03:10 ; Search time 141 Seconds
(without alignments)
1605.988 Million cell updates/sec

Title: US-10-730-010-2

Perfect score: 3404

Sequence: 1 MDKYDVIRKAGQAFGKAYL.....LCANDCSLKDWSEKEMELRT 640

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 1568699

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3404	100.0	640	14	US-10-243-735-2
2	3404	100.0	640	16	US-10-730-010-2
3	3081.5	90.5	683	9	US-09-940-921B-2
4	3081.5	90.5	889	17	US-10-618-941-94
5	2945	86.5	654	9	US-09-940-921B-4
6	2107.5	61.9	403	15	US-10-114-270-188
7	2102.5	61.8	399	15	US-10-114-270-186
8	1078	31.7	774	14	US-10-162-706-5
9	1072	31.5	1286	17	US-10-618-941-95
10	1062.5	31.2	616	14	US-10-243-735-4
11	1062.5	31.2	616	16	US-10-730-010-4
12	1060	31.1	1214	9	US-09-783-320-4
13	1060	31.1	1214	17	US-10-757-262-124

14	926.5	27.2	254	10	US-09-898-837A-35	Sequence 35, Appl
15	820.5	24.1	506	15	US-10-114-270-180	Sequence 180, Appl
16	815.5	24.0	345	9	US-09-870-962-6	Sequence 6, Appl
17	812	23.9	425	15	US-10-114-270-184	Sequence 184, Appl
18	810.5	23.8	489	15	US-10-114-270-182	Sequence 182, Appl
19	810.5	23.8	506	17	US-10-618-941-96	Sequence 96, Appl
20	810.5	23.8	506	17	US-10-757-262-118	Sequence 118, Appl
21	808.5	23.8	506	15	US-10-415-011-7	Sequence 7, Appl
22	731	21.5	459	9	US-09-771-161A-198	Sequence 198, Appl
23	675	19.8	850	15	US-10-425-114-56926	Sequence 56926, A
24	675	19.8	850	15	US-10-425-114-56928	Sequence 56928, A
25	663	19.5	841	14	US-10-198-070-52	Sequence 52, Appl
26	663	19.5	841	16	US-10-408-765A-1685	Sequence 1685, Appl
27	663	19.5	841	16	US-10-620-052A-32	Sequence 32, Appl
28	655	19.2	841	14	US-10-198-070-87	Sequence 87, Appl
29	645	18.9	416	9	US-09-731-231A-6	Sequence 6, Appl
30	645	18.9	416	16	US-10-751-985-6	Sequence 6, Appl
31	643	18.8	256	16	US-10-620-052A-48	Sequence 48, Appl
32	638.5	18.8	713	14	US-10-162-706-2	Sequence 2, Appl
33	638	18.7	260	9	US-09-731-231A-5	Sequence 5, Appl
34	638	18.7	260	16	US-10-751-985-5	Sequence 5, Appl
35	638	18.7	692	9	US-09-992-481-2	Sequence 2, Appl
36	638	18.7	692	14	US-10-434-034-2	Sequence 2, Appl
37	636	18.7	692	9	US-09-910-150-5	Sequence 5, Appl
38	636	18.7	692	15	US-10-377-097-5	Sequence 5, Appl
39	634	18.6	698	15	US-10-074-978A-144	Sequence 144, Appl
40	632.5	18.6	280	14	US-10-162-706-6	Sequence 6, Appl
41	632.5	18.6	460	14	US-10-162-706-4	Sequence 4, Appl
42	632.5	18.6	460	14	US-10-288-798-23	Sequence 23, Appl
43	632.5	18.6	460	15	US-10-362-893-23	Sequence 23, Appl
44	632	18.6	255	10	US-09-898-837A-36	Sequence 36, Appl
45	627.5	18.4	326	15	US-10-074-978A-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-10-243-735-2
; Sequence 2, Application US/10243735
; Publication No. US20030022341A1
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001212DIV
; CURRENT APPLICATION NUMBER: US/10/243,735
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Human
; US-10-243-735-2

Query Match 100.0%; Score 3404; DB 14; Length 640;
Best Local Similarity 100.0%; Pred No 2 6e-215;
Matches 640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MDKYDVIRKAGQAFGKAYLAKGSDSKHCVCIKINFEKMPIQEKASKEVILLERMKH	60
Db	1	MDKYDVIRKAGQAFGKAYLAKGSDSKHCVCIKINFEKMPIQEKASKEVILLERMKH	60
Qy	61	PNIVAFNSFOENGRPIFVNEYCDGDLMKRINRQGVLFSEQIILGWFIQISLGLKHIH	120
Db	61	PNIVAFNSFOENGRPIFVNEYCDGDLMKRINRQGVLFSEQIILGWFIQISLGLKHIH	120
Qy	121	DRKILHRDIKAQNFILSKNGWAKLGDGFGIARVLNNSMELARTICGTPTPYLSPEIQNK	180
Db	121	DRKILHRDIKAQNFILSKNGWAKLGDGFGIARVLNNSMELARTICGTPTPYLSPEIQNK	180

QY 181 YNNKTDIWSLGCVLVELCTLKHPFEGNNLQOLVLKICQAHFAPISPGFSRELHSLISQLF 240
DB 181 YNNKTDIWSLGCVLVELCTLKHPFEGNNLQOLVLKICQAHFAPISPGFSRELHSLISQLF 240
QY 241 QVSPDRPSINSILKRPFLNLI PKYLTPEVIQEFSSHMLICRAGAPASRHAGVQCK 300
DB 241 QVSPDRPSINSILKRPFLNLI PKYLTPEVIQEFSSHMLICRAGAPASRHAGVQCK 300
QY 301 IQKVRFGKCPPRSISVPIKRNAILHNRNWRPAGAKARSIMKIERPKIAAVCGHYD 360
DB 301 IQKVRFGKCPPRSISVPIKRNAILHNRNWRPAGAKARSIMKIERPKIAAVCGHYD 360
QY 361 YYAQLDMLRRRAHPSYHPIPOENTGVEDYGOETRHGSPSQWPAEYLQKFEAQYK 420
DB 361 YYAQLDMLRRRAHPSYHPIPOENTGVEDYGOETRHGSPSQWPAEYLQKFEAQYK 420
QY 421 VEKQGLRPSAEPNQRQELRNGEPRFQELPFRKNEMKEQYWKQLEETROQYVND 480
DB 421 VEKQGLRPSAEPNQRQELRNGEPRFQELPFRKNEMKEQYWKQLEETROQYVND 480
QY 481 MKEIRKMGREPEDIKDLKQMLQNTKESKNPQKYKAKKGVKFEINLDCISDENILQ 540
DB 481 MKEIRKMGREPEDIKDLKQMLQNTKESKNPQKYKAKKGVKFEINLDCISDENILQ 540
QY 541 BEEAMDIPNETLTPEDGMKFEYECVKEHGYDTDKAPEKLHCPAAFTLTWLSFLFLEY 600
DB 541 BEEAMDIPNETLTPEDGMKFEYECVKEHGYDTDKAPEKLHCPAAFTLTWLSFLFLEY 600
QY 601 SLPHFLLEKSPFSRHLLIEDLLCANDCSLKDWSEKEMELRT 640
DB 601 SLPHFLLEKSPFSRHLLIEDLLCANDCSLKDWSEKEMELRT 640

RESULT 2

US-10-730-010-2
; Sequence 2, Application US/10730010
; Publication No. US20040142366A1
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01212CIPDIV-II
; CURRENT APPLICATION NUMBER: US/10730.010
; CURRENT FILING DATE: 2003-12-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-730-010-2

Query Match 100.0%; Score 3404; DB 16; Length 640;
Best Local Similarity 100.0%; Pred. No. 2.6e-215;
Matches 640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKYDVIKAIQGGAFKAYLAGKSDSKHCVIKENFEMPIQEKASKKEVILKMKH 60
DB 1 MDKYDVIKAIQGGAFKAYLAGKSDSKHCVIKENFEMPIQEKASKKEVILKMKH 60
QY 61 PNIVAFNFSFQENGLRFTVMEYCDGGLMKRINRQGVLFSEDIQILGWVQVQISLGLKH 120
DB 61 PNIVAFNFSFQENGLRFTVMEYCDGGLMKRINRQGVLFSEDIQILGWVQVQISLGLKH 120
QY 121 DRKILHRDIKAQNTFSLKNGMVAKLGDFGIARVLNNSMELARTICIGTPYLSPEICQNK 180
DB 121 DRKILHRDIKAQNTFSLKNGMVAKLGDFGIARVLNNSMELARTICIGTPYLSPEICQNK 180
QY 181 YNNKTDIWSLGCVLVELCTLKHPFEGNNLQOLVLKICQAHFAPISPGFSRELHSLISQLF 240
DB 181 YNNKTDIWSLGCVLVELCTLKHPFEGNNLQOLVLKICQAHFAPISPGFSRELHSLISQLF 240

QY 241 QVSPDRPSINSILKRPFLNLI PKYLTPEVIQEFSSHMLICRAGAPASRHAGVQCK 300
DB 241 QVSPDRPSINSILKRPFLNLI PKYLTPEVIQEFSSHMLICRAGAPASRHAGVQCK 300
QY 301 IQKVRFGKCPPRSISVPIKRNAILHNRNWRPAGAKARSIMKIERPKIAAVCGHYD 360
DB 301 IQKVRFGKCPPRSISVPIKRNAILHNRNWRPAGAKARSIMKIERPKIAAVCGHYD 360
QY 361 YYAQLDMLRRRAHPSYHPIPOENTGVEDYGOETRHGSPSQWPAEYLQKFEAQYK 420
DB 361 YYAQLDMLRRRAHPSYHPIPOENTGVEDYGOETRHGSPSQWPAEYLQKFEAQYK 420
QY 421 VEKQGLRPSAEPNQRQELRNGEPRFQELPFRKNEMKEQYWKQLEETROQYVND 480
DB 421 VEKQGLRPSAEPNQRQELRNGEPRFQELPFRKNEMKEQYWKQLEETROQYVND 480
QY 481 MKEIRKMGREPEDIKDLKQMLQNTKESKNPQKYKAKKGVKFEINLDCISDENILQ 540
DB 481 MKEIRKMGREPEDIKDLKQMLQNTKESKNPQKYKAKKGVKFEINLDCISDENILQ 540
QY 541 BEEAMDIPNETLTPEDGMKFEYECVKEHGYDTDKAPEKLHCPAAFTLTWLSFLFLEY 600
DB 541 BEEAMDIPNETLTPEDGMKFEYECVKEHGYDTDKAPEKLHCPAAFTLTWLSFLFLEY 600
QY 601 SLPHFLLEKSPFSRHLLIEDLLCANDCSLKDWSEKEMELRT 640
DB 601 SLPHFLLEKSPFSRHLLIEDLLCANDCSLKDWSEKEMELRT 640

RESULT 3

US-09-940-921B-2
; Sequence 2, Application US/09940921B
; Patent No. US20020147320A1
; GENERAL INFORMATION:
; APPLICANT: Fiddle, Carl Johan
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: No. US20020147320A1el Human Kinase Proteins and Polynucleotides Br
; FILE REFERENCE: LEX-0227-USA
; CURRENT APPLICATION NUMBER: US/09/940.921B
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/229,280
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 683
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-940-921B-2

Query Match 90.5%; Score 3081.5; DB 9; Length 683;
Best Local Similarity 94.1%; Pred. No. 4.4e-194;
Matches 595; Conservative 2; Mismatches 4; Indels 31; Gaps 1;

QY 1 MDKYDVIKAIQGGAFKAYLAGKSDSKHCVIKENFEMPIQEKASKKEVILKMKH 60
DB 1 MDKYDVIKAIQGGAFKAYLAGKSDSKHCVIKENFEMPIQEKASKKEVILKMKH 60
QY 61 PNIVAFNFSFQENGLRFTVMEYCDGGLMKRINRQGVLFSEDIQILGWVQVQISLGLKH 120
DB 61 PNIVAFNFSFQENGLRFTVMEYCDGGLMKRINRQGVLFSEDIQILGWVQVQISLGLKH 120
QY 121 DRKILHRDIKAQNTFSLKNGMVAKLGDFGIARVLNNSMELARTICIGTPYLSPEICQNK 180
DB 121 DRKILHRDIKAQNTFSLKNGMVAKLGDFGIARVLNNSMELARTICIGTPYLSPEICQNK 180
QY 181 YNNKTDIWSLGCVLVELCTLKHPFEGNNLQOLVLKICQAHFAPISPGFSRELHSLISQLF 240
DB 181 YNNKTDIWSLGCVLVELCTLKHPFEGNNLQOLVLKICQAHFAPISPGFSRELHSLISQLF 240
QY 241 QVSPDRPSINSILKRPFLNLI PKYLTPEVIQEFSSHMLICRAGAPASRHAGVQCK 300

Db 241 QVSPDRPSINSLKRPFLNIPKYLTPDEVQESFHSMLICRAGAPASRHAGKVQCK 300
QY 301 IQKVRFRGKCPPRSISVIPKRNAILHRNWRPAGAKARSIMIERPKIAAVCGHYDY 360
Db 301 IQKVRFGKCPPRSISVIPKRNAILHRNWRPAGAKARSIMIERPKIAAVCGHYDY 360
QY 361 YQAOLDMLRRRAHAKPSVHPIPOENTGVEDYQGETRHGSPSPQWPAEYLQKFEAQYK 420
Db 361 YQAOLDMLRRRAHAKPSVHPIPOENTGVEDYQGETRHGSPSPQWPAEYLQKFEAQYK 420
QY 421 VEKQLGLRPSAEPNNQRLSNGEPRFOELPRKNEMKEQYWKOLEBIRQOYLND 480
Db 421 VEKQLGLRPSAEPNNQRLSNGEPRFOELPRKNEMKEQYWKOLEBIRQOYLND 480
QY 481 MKEIRKMGREPE-----DIEKDLKOMRLONTKE 509
Db 481 MKEIRKMGREPEENSISHTKTYLVKSNLPVHQDASEGEAPVQDIEKDLKOMRLONTKE 540
QY 510 SKNPEQKYKAGVKVFEINLDKICISDENILQEEBAMDIPNETLTFEDGMKFKEYECVKEH 569
Db 541 SKNPEQKYKAGVKVFEINLDKICISDENILQEEBAMDIPNETLTFEDGMKFKEYECVKEH 600
QY 570 GDYTDKAFKHLHCPAAFTLT 591
Db 601 GDYTDKAFKHLHCPAAGFTQT 622

RESULT 4
US-10-618-941-94
; Sequence 94, Application US/10618941
; Publication No. US20040197792A1
; GENERAL INFORMATION:
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERRARD
; APPLICANT: CAENEPEEL, SEAN
; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-0321
; CURRENT APPLICATION NUMBER: US/10/618,941
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/395,632
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 94
; LENGTH: 889
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-618-941-94

Query Match 90.5%; Score 3081.5; DB 17; Length 889;
Best Local Similarity 94.1%; Pred. No. 68-194;
Matches 585; Conservative 2; Mismatches 4; Indels 31; Gaps 1;

QY 1 MDKYDVTKAIGQAGFGKAYLAKGSDSKHCVIKEINFEKMPIQOEKASKEVILLERKMH 60
Db 58 MDKYDVTKAIGQAGFGKAYLAKGSDSKHCVIKEINFEKMPIQOEKASKEVILLERKMH 117
QY 61 PNIVAFNSFQENGRFLIYMEYCDGDLMKRINRQGVLFSDQILGWVQISLGLKHH 120
Db 118 PNIVAFNSFQENGRFLIYMEYCDGDLMKRINRQGVLFSDQILGWVQISLGLKHH 177
QY 121 DRKILHRDIKAQNIPLSKNGWAKLGDGFIARVLNNSMELARTCTGTPYLSPEICQNK 180
Db 178 DRKILHRDIKAQNIPLSKNGWAKLGDGFIARVLNNSMELARTCTGTPYLSPEICQNK 237
QY 181 YNNKTDIWSLGCVLVELCTLKHPFEGNNLQQLVLKICQAHFAPISPGFSRELHSLISOLF 240
Db 238 YNNKTDIWSLGCVLVELCTLKHPFEGNNLQQLVLKICQAHFAPISPGFSRELHSLISOLF 297
QY 241 QVSPDRPSINSLKRPFLNIPKYLTPDEVQESFHSMLICRAGAPASRHAGKVQCK 300
Db 298 QVSPDRPSINSLKRPFLNIPKYLTPDEVQESFHSMLICRAGAPASRHAGKVQCK 357

QY 301 IQKVRFRGKCPPRSISVIPKRNAILHRNWRPAGAKARSIMIERPKIAAVCGHYDY 360
Db 358 IQKVRFGKCPPRSISVIPKRNAILHRNWRPAGAKARSIMIERPKIAAVCGHYDY 417
QY 361 YQAOLDMLRRRAHAKPSVHPIPOENTGVEDYQGETRHGSPSPQWPAEYLQKFEAQYK 420
Db 418 YQAOLDMLRRRAHAKPSVHPIPOENTGVEDYQGETRHGSPSPQWPAEYLQKFEAQYK 477
QY 421 VEKQLGLRPSAEPNNQRLSNGEPRFOELPRKNEMKEQYWKOLEBIRQOYLND 480
Db 478 VEKQLGLRPSAEPNNQRLSNGEPRFOELPRKNEMKEQYWKOLEBIRQOYLND 537
QY 481 MKEIRKMGREPE-----DIEKDLKOMRLONTKE 509
Db 538 MKEIRKMGREPEENSISHTKTYLVKSNLPVHQDASEGEAPVQDIEKDLKOMRLONTKE 597
QY 510 SKNPEQKYKAGVKVFEINLDKICISDENILQEEBAMDIPNETLTFEDGMKFKEYECVKEH 569
Db 598 SKNPEQKYKAGVKVFEINLDKICISDENILQEEBAMDIPNETLTFEDGMKFKEYECVKEH 657
QY 570 GDYTDKAFKHLHCPAAFTLT 591
Db 658 GDYTDKAFKHLHCPAAGFTQT 679

RESULT 5
US-09-940-921B-4
; Sequence 4, Application US/09940921B
; Patent No. US20020147320A1
; GENERAL INFORMATION:
; APPLICANT: Fridde, Carl Johan
; APPLICANT: Hilbun, Brin
; APPLICANT: Nepomniichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: No. US20020147320A1 Human Kinase Proteins and Polynucleotides E
; FILE REFERENCE: LEX-0227-USA
; CURRENT APPLICATION NUMBER: US/09/940,921B
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/229,280
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 654
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-940-921B-4

Query Match 86.5%; Score 2945; DB 9; Length 654;
Best Local Similarity 94.3%; Pred. No. 3.9e-185;
Matches 564; Conservative 7; Mismatches 15; Indels 12; Gaps 4;

QY 1 MDKYDVTKAIGQAGFGKAYLAKGSDSKHCVIKEINFEKMPIQOEKASKEVILLERKMH 60
Db 1 MDKYDVTKAIGQAGFGKAYLAKGSDSKHCVIKEINFEKMPIQOEKASKEVILLERKMH 60
QY 61 PNIVAFNSFQENGRFLIYMEYCDGDLMKRINRQGVLFSDQILGWVQISLGLKHH 120
Db 61 PNIVAFNSFQENGRFLIYMEYCDGDLMKRINRQGVLFSDQILGWVQISLGLKHH 120
QY 121 DRKILHRDIKAQNIPLSKNGWAKLGDGFIARVLNNSMELARTCTGTPYLSPEICQNK 180
Db 121 DRKILHRDIKAQNIPLSKNGWAKLGDGFIARVLNNSMELARTCTGTPYLSPEICQNK 180
QY 181 YNNKTDIWSLGCVLVELCTLKHPFEGNNLQQLVLKICQAHFAPISPGFSRELHSLISOLF 240
Db 181 YNNKTDIWSLGCVLVELCTLKHPFEGNNLQQLVLKICQAHFAPISPGFSRELHSLISOLF 240
QY 241 QVSPDRPSINSLKRPFLNIPKYLTPDEVQESFHSMLICRAGAPASRHAGKVQCK 300
Db 241 QVSPDRPSINSLKRPFLNIPKYLTPDEVQESFHSMLICRAGAPASRHAGKVQCK 300


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; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Ji, Weizhen
; APPLICANT: Anderson, David W.
; APPLICANT: Liette, Mario W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Stone, David J.
; APPLICANT: MacDougall, John R.
; APPLICANT: Rothenberg, Mark E.
; TITLE OF INVENTION: NO. US20040030110A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-322C
; CURRENT APPLICATION NUMBER: US/10/114,270
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/281,086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SEQ ID NO 186
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-270-186

Query Match 61.8%; Score 2102.5; DB 15; Length 399;
Best Local Similarity 99.0%; Pred. No. 58-130; 0; Indels 3; Gaps 1;
Matches 398; Conservative 1; Mismatches 0;

QY 1 MDKYDVKAIGQAGAFKAYLAKGSDSKHCVCVKEINFEKMPIQEKEASKKEVILLERKMH 60
Db 1 MDKYDVKAIGQAGAFKAYLAKGSDSKHCVCVKEINFEK--QEKEASKKEVILLERKMH 57

QY 61 PNIVAFNFSQENGRLFIWMEYCDGDLMKRINRQGVLFSEDOILGHFWQISLGLKH 120
Db 58 PNIVAFNFSQENGRLFIWMEYCDGDLMKRINRQGVLFSEDOILGHFWQISLGLKH 117

QY 121 DRKILHRDIKAQNIPLSKNGWAKLDFGIARVLNNSMELARTCIGTPYLSPEICQNK 180
Db 118 DRKILHRDIKAQNIPLSKNGWAKLDFGIARVLNNSMELARTCIGTPYLSPEICQNK 177

QY 181 YNNKTDIWSLGCVLVELCTLKHPFEGNNLQQLVLKICQAHFAPISPGFSRELHLSISOLF 240
Db 178 YNNKTDIWSLGCVLVELCTLKHPFEGNNLQQLVLKICQAHFAPISPGFSRELHLSISOLF 237

QY 241 QVSPDRPSINSILKRPFLNLPKYLTPVEIQEFSHMLICRAGAPASRHAGKVQCK 300
Db 238 QVSPDRPSINSILKRPFLNLPKYLTPVEIQEFSHMLICRAGAPASRHAGKVQCK 297

QY 301 IQKVRFGKCPSPRSISVPIKRNAILHRNEWPPAGAKARSIKMIERPKIAAVCGHYDY 360
Db 298 IQKVRFGKCPSPRSISVPIKRNAILHRNEWPPAGAKARSIKMIERPKIAAVCGHYDY 357

QY 361 YYAQLDMLRRRAKHSYHPDQENTGVEDYGOETRHGSPSQ 402
Db 358 YYAQLDMLRRRAKHSYHPDQENTGVEDYGOETRHGSPSQ 399
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RESULT 8
US-10-162-706-5
; Sequence 5, Application US/10162706
; Publication No. US20030059918A1
; GENERAL INFORMATION:
; APPLICANT: Smolyar, Alex
; TITLE OF INVENTION: Regulation of Human Serine/Threonine
; TITLE OF INVENTION: Kinase
; FILE REFERENCE: 004974.00731
; CURRENT APPLICATION NUMBER: US/10/162,706
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/296,164
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/323,100
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 60/330,578
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/348,601
; PRIOR FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 774
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-706-5

Query Match 31.7%; Score 1078; DB 14; Length 774;
Best Local Similarity 36.4%; Pred. No. 2.3e-62;
Matches 260; Conservative 107; Mismatches 171; Indels 176; Gaps 21;

QY 1 MDKYDVKAIGQAGAFKAYLAKGSDSKHCVCVKEINFEKMPIQEKEASKKEVILLERKMH 60
Db 1 MEKYVRLQKIGEGSFGKAVLVKSTEDGRHYVKEINISMSDKERQESREVEAVLANVKH 60

QY 61 PNIVAFNFSQENGRLFIWMEYCDGDLMKRINRQGVLFSEDOILGHFWQISLGLKH 120
Db 61 PNIVQYKESPEENGSLYVMDYCEGGDLFRINAKGALFQEDQILDWFQICLALXHV 120

QY 121 DRKILHRDIKAQNIPLSKNGWAKLDFGIARVLNNSMELARTCIGTPYLSPEICQNK 180
Db 121 DRKILHRDIKAQNIPLSKNGWAKLDFGIARVLNNSMELARTCIGTPYLSPEICQNK 179

QY 181 YNNKTDIWSLGCVLVELCTLKHPFEGNNLQQLVLKICQAHFAPISPGFSRELHLSISOLF 240
Db 180 YNNKSDIWLGCVLVELCTLKHPFEGNNLQQLVLKICQAHFAPISPGFSRELHLSISOLF 239

QY 241 QVSPDRPSINSILKRPFLNLPKYLTPVEIQEFSHMLICRAGAPASRHAGKVQCK 285
Db 240 KRNPRDRPSINSILKRPFLNLPKYLTPVEIQEFSHMLICRAGAPASRHAGKVQCK 299

QY 286 ---APASRHAGKVQCKIQKVRFGKCPSPRSIS--VPIKRNAILHRNEWPP 333
Db 300 SSFVPAQKITKPAKYGVPVLTYYKYGDGKLLKPKPPKHAQHIQVKK---KNSGEERK 356

QY 334 PAG--AQKARSIKMIERPKIAAVCGHYDYVVAQDMLRR--RAH---KPSYHP--IPQE 348
Db 357 KMSEAAKRLRLEFIEKEKQKQIRFLKAEQMKRQKQLERINRAREQGNVLRAGG 416

QY 349 ---PKIAAVCGHYDYVVAQDMLRR--RAH---KPSYHP--IPQE 383
Db 417 SGEVKASFFGIGGAVSPSPCPGQYEHYHAIQDQVORLEADNEARWKGGIYGRWLPER 476

QY 384 NTG---VEDYGOETRHGSPSQWPAEYLRQKFAQYKLVKVE-----KQJGRPSS 431
Db 477 QKGLHAVERANQ-----VEBFLQRKRAMQNKARAEHVYVYVLAIRQLRQ--- 522

QY 432 AEPNYNORQELR-----SNGEERPFQELPRKMEKQEYVWKQLEBIRQOVLN 479
Db 523 ---NFNERQKITKAKLRGENKEADGCKGQEAT--BETDNR---LKMSLKAQTNARAVALK 575
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Db 357 KMSEAAKRRLEFIEKEKKQKQDQIRFLKAEQMKRQEKQRLERINRAEQGWRNVLRAGG 416
Qy 349 -----PKIAAVCGHYDYVYAAQLDMLRR-RAH-----KPSVHP--IPOE 383
Db 417 SGVKASFFGIGAVSPSPCSFPGQYEHYHALFDQMQLRAEDNEARWKGGIYGRWLPER 476
Qy 384 NTG---VEDYGQETHRGSPSPQWPAEYLQKPEAQYKLVKVE-----KQGLRPS 431
Db 477 QKGLAVERANQ-----VEEFLQKREAMQKARAEAGHVYVVLARLRQIRLQ--- 522
Qy 432 ASPNYNORCELRNGSEPRFQBLPFRKNEMKEQYWKQLEBIRQYLNDMKEIRKKMGRE 491
Db 523 ---NENERQOIKA-----LRGENKEADGTK-----GQE 548
Qy 492 PEDIEKDLKQMLQNTKESKNP-----EQYKAKGVKFEINLDKICISDENILOEEFAMD 546
Db 549 ATE-ETDMLKXVESLKAQTNAARAVALKEQLERKKEAYE--REKVVWEHLVARVKSSD 605
Qy 547 IPNETLTFEDG 557
Db 606 VPLPLELLETG 616

RESULT 11
US-10-730-010-4
; Sequence 4, Application US/10730010
; Publication No. US20040142366A1
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USBS
; FILE REFERENCE: CL001212CIPDIV-II
; CURRENT APPLICATION NUMBER: US/10/730,010
; CURRENT FILING DATE: 2003-12-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Mouse
US-10-730-010-4

Query Match 31.2%; Score 1062.5; DB 16; Length 616;
Best Local Similarity 36.7%; Pred. No. 1.8e-61;
Matches 246; Conservative 108; Mismatches 148; Indels 169; Gaps 18;
Qy 1 MDKYDVKAIGQAGAFKAYLAKGSDSKHCVKINEFEMPIQEKASKEVILEKMKH 60
Db 1 MEKYVRLQKIGESFGKAVLVKSTEDGRHYVKEINISRMDSKQESRREVAVLANMKH 60
Qy 61 PNIVAFNFSQENGELFIVMEYCDGDLMKRINRQGVLFSEDOILGWFVQISLGLKHII 120
Db 61 PNIVQKSFENGSLYIVMDYCEGGDLFKRINAGKALFQEDQILDWFVQICLAKHVI 120
Qy 121 DRKILHRDIKAQNIPLSKNGWAKLGDGFIARVLNNSMELARTICGTPTYYLSPEICQKP 180
Db 121 DRKILHRDIKSNIFLTNDGTV-QLGDGFIARVLNSTVELARTICGTPTYYLSPEICENKP 179
Qy 161 YNNKTIDWSLGCVLVELCTLKHPPFGNNLQQLVLKICQAHFAPISPGPSRELHLSOLF 240
Db 160 YNNKSDIHALGCVLYELCTLKHAFAGNKNLVLKIIISGSPFPVSPHYSLRSLLSOLF 239
Qy 241 QVSPDRPSINSILKRPFLNLIPLYLTPVETQEEFSHMLICRAG----- 285
Db 240 KENPRDRPSVNSILEKGFIAKRIEFLSPQLIAEFCLTKLSKGPQPLPKRPASGGV 299
Qy 286 -----APASHAGKWKQCKIQKVRFGKCPSPRSIS--VPIKRNAILHRNEWRP 333
Db 300 SSVFPAQKITKPAKYGVPLTYKYGDKKLLEKPPKPKHQAQHPVKK---MNSGGERK 356
Qy 334 PAG--AQXARSIKMLER----- 348

Db 357 KMSEAAKRRLEFIEKEKKQKQDQIRFLKAEQMKRQEKQRLERINRAEQGWRNVLRAGG 416
Qy 349 -----PKIAAVCGHYDYVYAAQLDMLRR-RAH-----KPSVHP--IPOE 383
Db 417 SGVKASFFGIGAVSPSPCSFPGQYEHYHALFDQMQLRAEDNEARWKGGIYGRWLPER 476
Qy 384 NTG---VEDYGQETHRGSPSPQWPAEYLQKPEAQYKLVKVE-----KQGLRPS 431
Db 477 QKGLAVERANQ-----VEEFLQKREAMQKARAEAGHVYVVLARLRQIRLQ--- 522
Qy 432 ASPNYNORCELRNGSEPRFQBLPFRKNEMKEQYWKQLEBIRQYLNDMKEIRKKMGRE 491
Db 523 ---NENERQOIKA-----LRGENKEADGTK-----GQE 548
Qy 492 PEDIEKDLKQMLQNTKESKNP-----EQYKAKGVKFEINLDKICISDENILOEEFAMD 546
Db 549 ATE-ETDMLKXVESLKAQTNAARAVALKEQLERKKEAYE--REKVVWEHLVARVKSSD 605
Qy 547 IPNETLTFEDG 557
Db 606 VPLPLELLETG 616

RESULT 12
US-09-783-320-4
; Sequence 4, Application US/09783320
; Patent No. US20020038011A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Turner, C. Alexander Jr
; APPLICANT: Zambrowicz, Brian
; TITLE OF INVENTION: No. US20020038011A1 Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0137-USA
; CURRENT APPLICATION NUMBER: US/09/783,320
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: US 60/183,582
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/184,014
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1214
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-783-320-4

Query Match 31.1%; Score 1060; DB 9; Length 1214;
Best Local Similarity 33.0%; Pred. No. 5.8e-61;
Matches 270; Conservative 128; Mismatches 203; Indels 218; Gaps 22;
Qy 1 MDKYDVKAIGQAGAFKAYLAKGSDSKHCVKINEFEMPIQEKASKEVILEKMKH 60
Db 1 MEKYVRLQKIGESFGKAVLVKSTEDGRQVVIKEINISRMSSKERESREAVAVLANMKH 60
Qy 61 PNIVAFNFSQENGRLFIVMEYCDGDLMKRINRQSGVLFSDDOILGWFVQISLGLKHII 120
Db 61 PNIVQKSFENGSLYIVMDYCEGGDLFKRINAGKGVLFQEDQILDWFVQICLAKHVI 120
Qy 121 DRKILHRDIKAQNIPLSKNGWAKLGDGFIARVLNNSMELARTICGTPTYYLSPEICQKP 180
Db 121 DRKILHRDIKSNIFLTNDGTV-QLGDGFIARVLNSTVELARTICGTPTYYLSPEICENKP 179
Qy 181 YNNKTIDWSLGCVLVELCTLKHPPFGNNLQQLVLKICQAHFAPISPGPSRELHLSOLF 240
Db 180 YNNKSDIHALGCVLYELCTLKHAFAGNKNLVLKIIISGSPFPVSPHYSLRSLYSOLF 239
Qy 241 QVSPDRPSINSILKRPFLNLIPLYLTPVETQEEFSHMLICRAG---PASHAG--- 293
Db 240 KENPRDRPSVNSILEKGFIAKRIEFLSPQLIAEFCLTKFSKFGSQPIPAKRPASGQNS 299

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OM protein - protein search, using sw model

Run on: November 12, 2004, 12:54:29 ; Search time 40 Seconds
(without alignments)

1061.088 Million cell updates/sec

Title: US-10-730-010-2

Perfect score: 3404

Sequence: 1 MDKYDVIRKAIQGGAFKAYL.....LCANDCSLKDWSEKEMELRT 640

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 segs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3404	100.0	640	4	US-09-873-404-2
2	3404	100.0	640	4	US-10-243-735-2
3	1062.5	31.2	616	4	US-09-873-404-4
4	1062.5	31.2	616	4	US-10-243-735-4
5	815.5	24.0	345	3	US-09-173-581-6
6	815.5	24.0	345	3	US-09-420-915-6
7	731	21.5	459	4	US-09-538-092-1182
8	655	19.2	841	4	US-09-538-092-1183
9	638	18.7	692	4	US-09-992-481-2
10	590	17.3	645	4	US-10-196-927-2
11	594	17.2	482	4	US-10-196-927-4
12	538.5	15.8	979	3	US-08-870-529-2
13	538.5	15.8	979	4	US-09-544-794-2
14	535.5	15.7	445	4	US-09-167-206-2
15	535.5	15.7	445	4	US-09-538-092-1181
16	512.5	15.1	699	3	US-09-457-040B-18
17	462.5	13.6	302	3	US-09-221-235-2
18	462.5	13.6	302	3	US-09-221-928-2
19	462.5	13.6	302	3	US-09-221-527-2
20	462.5	13.6	302	3	US-09-221-236-2
21	462.5	13.6	302	3	US-09-221-416-2
22	462.5	13.6	302	3	US-09-221-245-2
23	462.5	13.6	302	3	US-09-163-115-2
24	462.5	13.6	302	3	US-09-221-528-2
25	462.5	13.6	302	3	US-09-593-553-2
26	462.5	13.6	302	3	US-09-221-237-2
27	462.5	13.6	302	4	US-09-757-982-2

28	458.5	13.5	302	4	US-09-579-664B-9	Sequence 9, Appli
29	458.5	13.5	302	4	US-10-355-975A-9	Sequence 9, Appli
30	450.5	13.2	451	4	US-09-248-796A-18414	Sequence 18414, A
31	427	12.5	233	2	US-08-712-709-1	Sequence 1, Appli
32	427	12.5	233	3	US-09-111-444-1	Sequence 1, Appli
33	427	12.5	233	3	US-09-541-228-1	Sequence 1, Appli
34	415.5	12.2	647	3	US-09-031-563-7	Sequence 7, Appli
35	415.5	12.2	647	4	US-09-392-277-7	Sequence 7, Appli
36	415.5	12.2	647	4	US-09-258-000-7	Sequence 7, Appli
37	415.5	12.2	648	3	US-09-031-563-5	Sequence 5, Appli
38	415.5	12.2	648	4	US-09-392-277-5	Sequence 5, Appli
39	415.5	12.2	648	4	US-09-258-000-5	Sequence 5, Appli
40	415.5	12.2	1115	4	US-10-335-711-2	Sequence 2, Appli
41	415.5	12.2	1315	3	US-09-031-563-2	Sequence 2, Appli
42	415.5	12.2	1315	3	US-09-293-505-10	Sequence 10, Appli
43	415.5	12.2	1315	4	US-09-392-277-2	Sequence 2, Appli
44	415.5	12.2	1315	4	US-09-258-000-2	Sequence 2, Appli
45	415.5	12.2	1315	4	US-09-660-939A-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-09-873-404-2
; Sequence 2, Application US/09873404
; Patent No. 6500656
; GENERAL INFORMATION:
; APPLICANT: WESTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CUC01212-CIP
; CURRENT APPLICATION NUMBER: US/09/873,404
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Human
; US-09-873-404-2

Query Match						100.0%; Score 3404; DB 4; Length 640;
Best Local Similarity						100.0%; Pred. No. 2.3e-272;
Matches						640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	MDKYDVIRKAIQGGAFKAYLAKGSDSKHCVCVKEINFEKMPIQEKASKEVILLEKMKH	60			
Db	1	MDKYDVIRKAIQGGAFKAYLAKGSDSKHCVCVKEINFEKMPIQEKASKEVILLEKMKH	60			
Qy	61	PNIVAFNSFOENGRLFIWMEYCDGDLMKRINRQGVLPSEDOILGWFVQISLGLKHH	120			
Db	61	PNIVAFNSFOENGRLFIWMEYCDGDLMKRINRQGVLPSEDOILGWFVQISLGLKHH	120			
Qy	121	DRKTLHEDIKAQIFLSKNGWAKLGDGFIARVNNNSMELARTCIGTPYYLSPEIQNKP	180			
Db	121	DRKTLHEDIKAQIFLSKNGWAKLGDGFIARVNNNSMELARTCIGTPYYLSPEIQNKP	180			
Qy	181	YNNKTDIWSLGCVLVELCTLKHFPFGNNLOQLVLIKQAHFAPISFGFSELHSLISQLP	240			
Db	181	YNNKTDIWSLGCVLVELCTLKHFPFGNNLOQLVLIKQAHFAPISFGFSELHSLISQLP	240			
Qy	241	QVSPDRPSPNSILKRPFLENLPKYLTPVEIQEFSHMLICRAGAPASHAGKVKQCK	300			
Db	241	QVSPDRPSPNSILKRPFLENLPKYLTPVEIQEFSHMLICRAGAPASHAGKVKQCK	300			
Qy	301	IQVRFKGCPPSRISVPIKRNAILHRNWRPPAGAKARSIMTERPKIAVCGHYDY	360			
Db	301	IQVRFKGCPPSRISVPIKRNAILHRNWRPPAGAKARSIMTERPKIAVCGHYDY	360			
Qy	361	YYAOLDMLRRRAKPSVHPPIQENTGVEDYQETRHGSPSQWPAEYLQKFEAQYKLL	420			

Db 361 YYAQLDMLRRRAHPSYHP1PQENTGVEDYQETRHGSPSQWPAEYLRQKFAQQYK 420
QY 421 VEKQLGLRPSAEPNYNQRELRSNGEPRFQELPFRKNEMKEQYWKQLEIRQQVYND 480
Db 421 VEKQLGLRPSAEPNYNQRELRSNGEPRFQELPFRKNEMKEQYWKQLEIRQQVYND 480
QY 481 MKEIRKMGREPEDIEKDLKQMLQNTKESKNPEQYKAKKGKVFENLNDKCI SDENILQ 540
Db 481 MKEIRKMGREPEDIEKDLKQMLQNTKESKNPEQYKAKKGKVFENLNDKCI SDENILQ 540
QY 541 BEEAMDIPNEILTLEDGKMKFKEVCVKEHGDYTDKAFKHLCPAAFTLTWLSFLFLEY 600
Db 541 BEEAMDIPNEILTLEDGKMKFKEVCVKEHGDYTDKAFKHLCPAAFTLTWLSFLFLEY 600
QY 601 SLPHFLLEKSPFSRHLIEDLLCANDCSLKDWSEKEMELRT 640
Db 601 SLPHFLLEKSPFSRHLIEDLLCANDCSLKDWSEKEMELRT 640
RESULT 2
US-10-243-735-2
; Sequence 2, Application US/10243735
; Patent No. 6706510
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001212D1V
; CURRENT APPLICATION NUMBER: US/10/243,735
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Human
US-10-243-735-2
Query Match 100.0%; Score 3404; DB 4; Length 640;
Best Local Similarity 100.0%; Pred. NO. 2.3e-272;
Matches 640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDKYDV1KAIQGAGFKAYLAKGSDSKHCVIKKEINFEKMPIQKEASKEVILLEMKH 60
Db 1 MDKYDV1KAIQGAGFKAYLAKGSDSKHCVIKKEINFEKMPIQKEASKEVILLEMKH 60
QY 61 PNIVAFNSFOENGRLEFVMEYCDGGDLMKRINRQGVLFSEDOILGWFWQISLGLKH 120
Db 61 PNIVAFNSFOENGRLEFVMEYCDGGDLMKRINRQGVLFSEDOILGWFWQISLGLKH 120
QY 121 DRKILHRDIKAQNTFLSKNGVAKLGDGFIARVLNNSMELARTCIGTPPYLSPEICQKP 180
Db 121 DRKILHRDIKAQNTFLSKNGVAKLGDGFIARVLNNSMELARTCIGTPPYLSPEICQKP 180
QY 181 YNNKTDIWSLGCVLVEYELCTLKHPEGNLQOLVLIQAHFAPISPGFSRELHSLISOLF 240
Db 181 YNNKTDIWSLGCVLVEYELCTLKHPEGNLQOLVLIQAHFAPISPGFSRELHSLISOLF 240
QY 241 QVSPDRPSINSILKRPFLNLIPIKYLTPVIOEERSHMLICRAGAPASHAGKVVQCK 300
Db 241 QVSPDRPSINSILKRPFLNLIPIKYLTPVIOEERSHMLICRAGAPASHAGKVVQCK 300
QY 301 IQKVRFRGKCPPRSRI SVPIKRNAILHRNWRPPAGAKARSIMIERPKIAAVCGHYD 360
Db 301 IQKVRFRGKCPPRSRI SVPIKRNAILHRNWRPPAGAKARSIMIERPKIAAVCGHYD 360
QY 361 YYAQLDMLRRRAHPSYHP1PQENTGVEDYQETRHGSPSQWPAEYLRQKFAQQYK 420
Db 361 YYAQLDMLRRRAHPSYHP1PQENTGVEDYQETRHGSPSQWPAEYLRQKFAQQYK 420
QY 421 VEKQLGLRPSAEPNYNQRELRSNGEPRFQELPFRKNEMKEQYWKQLEIRQQVYND 480

Db 421 VEKQLGLRPSAEPNYNQRELRSNGEPRFQELPFRKNEMKEQYWKQLEIRQQVYND 480
QY 481 MKEIRKMGREPEDIEKDLKQMLQNTKESKNPEQYKAKKGKVFENLNDKCI SDENILQ 540
Db 481 MKEIRKMGREPEDIEKDLKQMLQNTKESKNPEQYKAKKGKVFENLNDKCI SDENILQ 540
QY 541 BEEAMDIPNEILTLEDGKMKFKEVCVKEHGDYTDKAFKHLCPAAFTLTWLSFLFLEY 600
Db 541 BEEAMDIPNEILTLEDGKMKFKEVCVKEHGDYTDKAFKHLCPAAFTLTWLSFLFLEY 600
QY 601 SLPHFLLEKSPFSRHLIEDLLCANDCSLKDWSEKEMELRT 640
Db 601 SLPHFLLEKSPFSRHLIEDLLCANDCSLKDWSEKEMELRT 640
RESULT 3
US-09-873-404-4
; Sequence 4, Application US/09873404
; Patent No. 650656
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001212-CIP
; CURRENT APPLICATION NUMBER: US/09/873,404
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Mouse
US-09-873-404-4
Query Match 31.2%; Score 1062.5; DB 4; Length 616;
Best Local Similarity 36.7%; Pred. NO. 3.5e-79;
Matches 246; Conservative 108; Mismatches 148; Indels 169; Gaps 18;
QY 1 MDKYDV1KAIQGAGFKAYLAKGSDSKHCVIKKEINFEKMPIQKEASKEVILLEMKH 60
Db 1 MEKYVRLQIKIGEGFGKAVLVKSTEDGRHYVIKINISRMDSKQSRREAVLANMKH 60
QY 61 PNIVAFNSFOENGRLEFVMEYCDGGDLMKRINRQGVLFSEDOILGWFWQISLGLKH 120
Db 61 PNIVQKESFEENGSLYIMDYCEGDLFKRINAQKALFOEDQILDWFWQICLALKHVH 120
QY 121 DRKILHRDIKAQNTFLSKNGVAKLGDGFIARVLNNSMELARTCIGTPPYLSPEICQKP 180
Db 121 DRKILHRDIKQNTFLTKDGTV-QLGDFGIARVLNNSMELARTCIGTPPYLSPEICENKP 179
QY 181 YNNKTDIWSLGCVLVEYELCTLKHPEGNLQOLVLIQAHFAPISPGFSRELHSLISOLF 240
Db 180 YNNKSDIHALGCVLVEYELCTLKHPEAGNMKNLVLISSGPPVSPHVSYDLRSLLSOLF 239
QY 241 QVSPDRPSINSILKRPFLNLIPIKYLTPVIOEERSHMLICRAGAPASHAGKVVQCK 285
Db 240 KENPRDRPSVNSILEKGFIAKRIEFLSPQIABEFCFLKLSKFGPQLPGKRPASQGV 299
QY 286 -----APASHAGKVVQCKIKOVRFRGKCPPRSRI SVPIKRNAILHRNWRP 333
Db 300 SSFVPAQKITPAKYGVPLYIKYVKGLLEKPPKPKGQAHQIPVKK---MNSGERK 356
QY 334 PAG--AQKARSIMIER----- 348
Db 357 KMSEAAKRRLEFIEKKQKQDQIRFLKAEQMKRQEKRLERINRAREQGRNVLRAGG 416
QY 349 -----PKIAAVCGHYDYVAQLOMLRR-RAH-----KPSYHP--IPOE 383
Db 417 SGEVKASFFGIGGAVSPSPRQCYEYHYHAI PQMORLAEADNEARKWGIQWMLPER 476
QY 384 NTG---VEDYQETRHGSPSQWPAEYLRQKFAQQYK 431

Db 477 QKCHLAVERANQ-----VEEFLQKREAMONKARAEHGVVYLARLQIRIQ--- 522
Qy 432 AEPNYNQRELRSNGEPRFQELPFRKNEMKEQYWKQLEIRQOYLNDMKEIRKMGRE 491
Db 523 ---NFEROQIKAK-----LRGENKEADGTK-----GOE 548
Qy 492 PEDIEKDLQMRLONTKESKNP-----BQYKAKKGKGVKFEINLDKICISDENILQEBEAMD 546
Db 549 ATE-ETDMRLKKVESLKAQTNARAVALKEQLERKKEAYE--REKKVWEEHLVARVKSSD 605
Qy 547 IPNETLTFEDG 557
Db 606 VPLPLELLEGTG 616

RESULT 4

US-10-243-735-4
; Sequence 4, Application US/10243735
; Patent No. 6706510
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001212DIV
; CURRENT APPLICATION NUMBER: US/10/243,735
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Mouse
US-10-243-735-4

Query Match 31.2%; Score 1062.5; DB 4; Length 616;
Best Local Similarity 36.7%; Pred. No. 3.5e-79;
Matches 246; Conservative 108; Mismatches 148; Indels 169; Gaps 18;

Qy 1 MDKYDVIKAIQAGAFKAYLAKGSKDSKHCVIKEINFEKMPIOEKEASKKEVILLKMKH 60
Db 1 MEKYVRLQKIGSGFGKAILVKTSTEDGRHYVKEINISRMDSKEREERREAVLANMKH 60
Qy 61 PNIVAFNFSQENGRLFIYMEYCDGDLMKRINRQGVLFSEDIQILGWFOISLGLKHH 120
Db 61 PNIVQKESFEENGSLIYMDYCEGDLFKRNAQKALFQSDQILDWFOICLALKEVH 120
Qy 121 DRKILHRDIKAONIPLSKNGMVAKLGDGFIARVNLNNSMELARTCTGTPYLSPEICNKP 180
Db 121 DRKILHRDIKSONIFLTKDGTGTV-QLGDFGIARVNLNSTVELARTCTGTPYLSPEICNKP 179
Qy 181 YNNKTDIWSLGCVLVELCTLKHFPFEGNLLQOLVLIKCOAHFAPISGPFSSRELHSLISOLF 240
Db 180 YNNKSDIWSLGCVLVELCTLKHAFEGNMKNVLVLAISGSPFPVSPHYSDRLSLSOLF 239
Qy 241 QVSPDRPSINSILKRPFLNLIPIKYLTPVTOEBSHMLICRAG----- 285
Db 240 KENPRDRPSVNSILEKGFIAKRIEFLSPOLIAEFCFLKTLKSPQPLPKGRPASGQGV 299
Qy 286 -----APASHAGKVVQCKIQVFRPGKCPPRSIS--VPIKRNAILHREWRP 333
Db 300 SSVFPAQKITKPAAYKGVPLTYKKGDKKLEKKPPPHKQAHQIPVK--MNSGEERK 356
Qy 334 PAG--AQKARSIMIER----- 348
Db 357 KMSEEAARKRRLEFIEKEKKQDQIRFLKAEQKQEKQRLERINRAREQGWNVIRAGG 416
Qy 349 -----PKTAAVGHYDYVYQALMLRR-RAH-----KPSVHP--IQE 383
Db 417 SEVKASPTGIGVAVSPSCSPRGQVEHYHAIFDQMQLRABDNARWKGGIYGRWLPER 476
Qy 384 NTG----VEDYGOETRHGSPSPQWPAEYLQKPEAQYKLVKE-----KQLGRPSS 431

Db 477 QKCHLAVERANQ-----VEEFLQKREAMONKARAEHGVVYLARLQIRIQ--- 522
Qy 432 AEPNYNQRELRSNGEPRFQELPFRKNEMKEQYWKQLEIRQOYLNDMKEIRKMGRE 491
Db 523 ---NFEROQIKAK-----LRGENKEADGTK-----GOE 548
Qy 492 PEDIEKDLQMRLONTKESKNP-----BQYKAKKGKGVKFEINLDKICISDENILQEBEAMD 546
Db 549 ATE-ETDMRLKKVESLKAQTNARAVALKEQLERKKEAYE--REKKVWEEHLVARVKSSD 605
Qy 547 IPNETLTFEDG 557
Db 606 VPLPLELLEGTG 616
RESULT 5
US-09-173-581-6
; Sequence 6, Application US/09173581A
; Patent No. 6013455
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Gorgone, Gina
; APPLICANT: Azimzal, Yalda
; APPLICANT: Lu, Aina
; TITLE OF INVENTION: Protein Kinase Homologs
; FILE REFERENCE: PP-0614 US
; CURRENT APPLICATION NUMBER: US/09/173,581A
; CURRENT FILING DATE: 1998-10-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1567782
US-09-173-581-6

Query Match 24.0%; Score 815.5; DB 3; Length 345;
Best Local Similarity 45.1%; Pred. No. 3.7e-59;
Matches 173; Conservative 56; Mismatches 80; Indels 75; Gaps 7;

Qy 1 MDKYDVIKAIQAGAFKAYLAKGSKDSKHCVIKEINFEKMPIOEKEASKKEVILLKMKH 60
Db 1 MEKYVRLQKIGSGFGKAILVKTSTEDGRQYVKEINISRMSSKEREERREAVLANMKH 60
Qy 61 PNIVAFNFSQENGRLFIYMEYCDGDLMKRINRQGVLFSEDIQILGWFOISLGLKHH 120
Db 61 PNIVQYRESF-----EGILDWFOICLALKEVH 88
Qy 121 DRKILHRDIKAONIPLSKNGMVAKLGDGFIARVNLNNSMELARTCTGTPYLSPEICNKP 180
Db 89 DRKILHRDIKSONIFLTKDGTGTV-QLGDFGIARVNLNSTVELARTCTGTPYLSPEICNKP 147
Qy 181 YNNKTDIWSLGCVLVELCTLKHFPFEGNLLQOLVLIKCOAHFAPISGPFSSRELHSLISOLF 240
Db 148 YNNKSDIWSLGCVLVELCTLKHAFEGNMKNVLVLAISGSPFPVSPHYSDRLSLSOLF 207
Qy 241 QVSPDRPSINSILKRPFLNLIPIKYLTPVTOEBSHMLICRAG---PASHAG--- 293
Db 208 KENPRDRPSVNSILEKGFIAKRIEFLSPOLIAEFCFLKTLKSPQPLPKGRPASGQNS 267
Qy 294 -KVQCKIQKQVFRPGKCPPRSISVPI-----KRNAILHREWRP----- 334
Db 268 ISVMPAQKITK-----PAAYKGVPLTYKKGDKKLEKKPPPHKQAHQIPKEKVT 319
Qy 335 -----AGAQKARSIMIERPK 350

Db 320 GEERRKISEEAAKRRLEFIEKDK 343

RESULT 6

US-09-420-915-6

; Sequence 6, Application US/09420915

; Patent No. 6264947

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Tang, Y. Tom

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Yue, Henry

; APPLICANT: Guegler, Karl J.

; APPLICANT: Corley, Neil C.

; APPLICANT: Gorgone, Gina

; APPLICANT: Azimzai, Valda

; APPLICANT: Lu, Aina

; TITLE OF INVENTION: Protein Kinase Homologs

; FILE REFERENCE: PF-0614 US

; CURRENT APPLICATION NUMBER: US/09/420,915

; CURRENT FILING DATE: 1999-10-20

; EARLIER APPLICATION NUMBER: US 09/173,581

; EARLIER FILING DATE: 1998-10-15

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PERL Program

; SEQ ID NO 6

; LENGTH: 345

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: 1567782

US-09-420-915-6

Query Match 24.0%; Score 815.5; DB 3; Length 345;
Best Local Similarity 45.1%; Pred. No. 3.7e-59;
Matches 173; Conservative 56; Mismatches 80; Indels 75; Gaps 7;

Qy 1 MDKVDVTKATGGAFGKAYLAGKSDSKVCHVKEINFEKMPIOEKASKKEVILLKMKH 60

Db 1 MEKVRLQKIGEGFGKAILVKTSTEDGRQYVKEINISRMSSKERESREAVLANMKH 60

Qy 61 PNIVAFNFSQENGRLEFIVMEYCDGDLMKRINRQGVLPSEDIQICWFVQISLGLKHIH 120

Db 61 PNIVQYRESP.....EGILDWFVQICLAKVH 88

Qy 121 DRKILHRDIKAQNIIFLSKNGVAKLDFGIARVLNNSMELARTCIGTPYYLSPEICNKP 180

Db 89 DRKILHRDIKSONIFLTQDGTV-QLGDFGIARVLNSTVELARTCIGTPYYLSPEICENKP 147

Qy 181 YNNKTDLSLGCVLVELCTLKHPEGNLQVLKICQAHFAPISPCFSRELHSLISQLF 240

Db 148 YNNKSDWLALGCVLYELCTLKHPEAGSMKNLVLIISGSPFVSLHYSDLSLSQLF 207

Qy 241 QVSPDRPSINSILKRPFLENLIPKYLTPBVIQEEFESHMLICRAGA---PASRHAG---- 293

Db 208 KRNPRDRPSVNSILEKGFIAKRIEKLPLSLIAEEFCLTKFSKGSQPIPAKRPASQNS 267

Qy 294 -KVQKCKIQVFRGKCPPRSISVPI-----KRNAILHRNWRP----- 334

Db 268 ISVPAQKIKT-----PAAKYGIPLAYKYGDKLHKPLQKHQAHOPTPEKRVNT 319

Qy 335 -----AGAKQARSIMKIERPK 350

Db 320 GEERRKISEEAAKRRLEFIEKDK 343

RESULT 7

US-09-538-092-1182

; Sequence 1182, Application US/09538092

; Patent No. 6753314

; GENERAL INFORMATION:

; APPLICANT: Giot, Loic

; APPLICANT: Mansfield, Traci A.

; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

; FILE REFERENCE: 15966-542

; CURRENT APPLICATION NUMBER: US/09/538,092

; CURRENT FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: 60/127,352

; PRIOR FILING DATE: 1999-04-01

; PRIOR APPLICATION NUMBER: 60/178,965

; PRIOR FILING DATE: 2000-02-01

; NUMBER OF SEQ ID NOS: 1387

; SOFTWARE: CuraPatSeqFormat Version 0.9

; SEQ ID NO 1182

; LENGTH: 459

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (0)...(0)

; OTHER INFORMATION: Polypeptide Accession Number P51956

US-09-538-092-1182

Query Match 21.5%; Score 731; DB 4; Length 459;
Best Local Similarity 33.8%; Pred. No. 5.2e-52;
Matches 175; Conservative 79; Mismatches 151; Indels 112; Gaps 13;

Qy 49 KKEVILLKMKHPNIVAFNFSQENGRLEFIVMEYCDGDLMKRINRQGVLPSEDIQILGW 108

Db 1 RKEAVLSARKMKHPNIVAFNFSQENGRLEFIVMEYCDGDLMKRINRQGVLPSEDIQILGW 60

Qy 109 FVOISLGLKHIHDKILHRDIKAQNIIFLSKNGVAKLDFGIARVLNNSMELARTCIGTP 168

Db 61 PTOMCLGVNHHKXVLRHDIKSNIFLTQNGKV-KLGDGFSARLLSNPMAFATYVGT 119

Qy 169 YLSPEICQNKYPNNKTDIWSLGCVLVELCTLKHPEGNLQVLKICQAHFAPISPGF 228

Db 120 YVVPPEIWENLPYNNKSDIWSLGCILVELCTLKHPEFQANSWKNILKVQCGCISPLPSHY 179

Qy 229 SRELHSLISQLFQVSPDRPSINSILKRPFLENLIPKYLTPBVIQEEFESHMLICRAGA 288

Db 180 SYELOFLVQKQKPNRSHRPSATLLSRGIVARLVQKCLPPEIIVE----- 225

Qy 289 SRHAGKVQKCKIQVFRGKCPPRSISVPIKENAILHRNWRPAPAGAKQARSIMKIER 348

Db 226 --YGEVLEIEIKNSKHNTPRKKTNPRIALGNEASTVQEEQDRKGS----- 272

Qy 349 PKIAAVCGHYDYAQLDMLRRRAKPSYHPIPOENTGVEDYQGETRHGSPS-----QWP 404

Db 273 -----HTDLESINENLVESALRRVNEEKG--NKSVHLRRASPNLHRRQW- 316

Qy 405 AEYLQKPEAQYKLVKVEKQLGRPSSAEFNNQORQLRSN--GEEPR-FOELPFRKNEM 461

Db 317 -----EKNV---PNTALTALENASILTSLTAEDDRGGSGVSKNTT 356

Qy 462 KEQEVWVKOLEIRQYLNDMKE-----IRKMGRE----- 491

Db 357 RKQ--W--LKETPTDLNKLKADLSLAFQTYTIRPFGSEGLKPLSEATEASDVGG 412

Qy 492 -----PEDTEKDLQKWLQNTKESKNKPEQYKAKK 521

Db 413 HDSVILDPERLEPGLDEEDTDFEEDDNDPWSLKK 449

RESULT 8

US-09-538-092-1183

; Sequence 1183, Application US/09538092

; Patent No. 6753314

; GENERAL INFORMATION:

; APPLICANT: Giot, Loic

; APPLICANT: Mansfield, Traci A.

; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

; FILE REFERENCE: 15966-542

; CURRENT APPLICATION NUMBER: US/09/538,092

; CURRENT FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: 60/127,352


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; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 645
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-196-927-2

Query Match      17.3%; Score 590; DB 4; Length 645;
Best Local Similarity 28.4%; Pred. No. 3.6e-40;
Matches 161; Conservative 106; Mismatches 157; Indels 102; Gaps 17;

QY 3 KYDVKAIGQAGAFKAYLA---KKSQSKHCIVKEINFEKMPIOEKASKEVILLKMK 59
Db 28 RYVLQKLGSGSFGTVYLVSDKAKRGEELKVLKEISVGLNPNETVQANLEAQLSKLD 87
QY 60 HPNTVAFNFSQENGRLPIVMVEYCDGDLMKRIN--RQGVLFSEDDQILGWFOVLSGLK 117
Db 88 HPAIVKHFASVFEQDNFCIITEYCEGRDLDDKIQEYKQAGKIPENQIIEFWFIQLLQVD 147
QY 118 HIHDKILHRDIKAQNTIFLSKNGMVAKLGDGFIARVLNNSMELARTCIGTPYVLSPEICQ 177
Db 148 YMHERRILHRDLKSKNVLKNN--LLKIGDFGVSRLLMGSCDLATTTLTGTTHYMSPEALK 205
QY 178 NKPYNNKTDIWSLGCVLVELCTLKHPPGNNLQOLVKICQAHFAPISPGFSRELHSLIS 237
Db 206 HQGYDTRSDIWSLACILYEMCCMHAFAGSNFLSIVLKIVEGTPSPUPERYPKELNAIME 265
QY 238 QLFQVSPDRPSINSILKRPF---LENLIPKY--LTPE---VIOEFSHMLICRAGAP 287
Db 266 SMLNKNPSLRPSATEILKIPYLDQQLNLMCRYSEMTELDKNLDCQKEAAHII----- 318
QY 288 ASRHAGKVQCKTKQVFRG---KCPPRSISVPIKRNAILHNRNWRPAGAKARSIK 344
Db 319 -----NAMQKRIHQTLRALSEVQKMTFRERMRLR-----KLOAADERKARKLK 361
QY 345 MIERPKIAAVGCHDYVYVYQALDMLRRRAHKPSYHPIPOENTGVEDYQETRHGSPSQWP 404
Db 362 KIVEEK-----YEENSKRMQELSRNFQOLSVDVLHEKTHLKG----- 399
QY 405 AYLQKFEAQYKLVKVEKQLGLRPSABPNYNQORQLRNGEPRFOELPFRKNEKQ 464
Db 400 ---MEEKEQPEGLRSCSPQ-----DDEERWQGRSE---ESDEPTLENLP----- 439
QY 465 EYWKOLBEIRQYLNDMKEIRKMGREPEDEIKDLQMRLQNTKESKNPKYKAKKGVK 524
Db 440 -----ESQIPSMDLHELESI-----VEDATSDLGYHEI---PEDPLVABEYVADAFDS 485
QY 525 FEINLDCISDENILQEEAAWIPNE 550
Db 486 YCVESDE--BEEETALERPEKEIRNE 509

RESULT 11
US-10-196-927-4
; Sequence 4, Application US/10196927
; Patent No. 6797510
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6797510el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0348-USA
; CURRENT APPLICATION NUMBER: US/10196,927
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 60/293,248
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 482
; TYPE: PRT
```

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; ORGANISM: homo sapiens
US-10-196-927-4

Query Match      17.2%; Score 584; DB 4; Length 482;
Best Local Similarity 29.2%; Pred. No. 7.5e-40;
Matches 149; Conservative 94; Mismatches 164; Indels 104; Gaps 14;

QY 3 KYDVKAIGQAGAFKAYLA---KKSQSKHCIVKEINFEKMPIOEKASKEVILLKMK 59
Db 28 RYVLQKLGSGSFGTVYLVSDKAKRGEELKVLKEISVGLNPNETVQANLEAQLSKLD 87
QY 60 HPNTVAFNFSQENGRLPIVMVEYCDGDLMKRIN--RQGVLFSEDDQILGWFOVLSGLK 117
Db 88 HPAIVKHFASVFEQDNFCIITEYCEGRDLDDKIQEYKQAGKIPENQIIEFWFIQLLQVD 147
QY 118 HIHDKILHRDIKAQNTIFLSKNGMVAKLGDGFIARVLNNSMELARTCIGTPYVLSPEICQ 177
Db 148 YMHERRILHRDLKSKNVLKNN--LLKIGDFGVSRLLMGSCDLATTTLTGTTHYMSPEALK 205
QY 178 NKPYNNKTDIWSLGCVLVELCTLKHPPGNNLQOLVKICQAHFAPISPGFSRELHSLIS 237
Db 206 HQGYDTRSDIWSLACILYEMCCMHAFAGSNFLSIVLKIVEGTPSPUPERYPKELNAIME 265
QY 238 QLFQVSPDRPSINSILKRPF---LENLIPKY--LTPE---VIOEFSHMLICRAGAP 287
Db 266 SMLNKNPSLRPSATEILKIPYLDQQLNLMCRYSEMTELDKNLDCQKEAAHII----- 318
QY 288 ASRHAGKVQCKTKQVFRG---KCPPRSISVPIKRNAILHNRNWRPAGAKARSIK 344
Db 319 -----NAMQKRIHQTLRALSEVQKMTFRERMRLR-----KLOAADERKARKLK 361
QY 345 MIERPKIAAVGCHDYVYVYQALDMLRRRAHKPSYHPIPOENTGVEDYQETRHGSPSQWP 404
Db 362 KIVEEK-----YEENSKRMQELSRNFQOLSVDVLHEKTHLKG----- 399
QY 405 AYLQKFEAQYKLVKVEKQLGLRPSABPNYNQORQLRNGEPRFOELPFRKNEKQ 458
Db 400 ---MEEKEQPEGLRSCSPQ-----DDEERWQGRSE---ESDEPTLENLPESQIPSM 448
QY 459 -----NEMKEQYEWK 468
Db 449 LHELESIVEDATSDLGVDNCLISLDEYWK 479

RESULT 12
US-08-870-529-2
; Sequence 2, Application US/08870529
; Patent No. 6080557
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Virca, G. Duke
; APPLICANT: Bird, Timothy A.
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: IL-1/TNF-(-ACTIVATED KINASE (ITAK),
; NUMBER OF INVENTION: AND METHODS OF MAKING AND USING THE SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/870,529
; APPLICATION NUMBER: US/08/870,529
; FILING DATE: 06-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
```

NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 979 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-870-529-2

Query Match 15.8%; Score 538.5; DB 3; Length 979;
Best Local Similarity 36.1%; Pred. No. 1.1e-35;
Matches 116; Conservative 61; Mismatches 121; Indels 23; Gaps 5;

QY 4 YDVIKAIQGGAFKAYLAKGSDSKHCIVKINFEKMPIOQEASKEVILLESKHPNI 63
DB 52 YPIRVLGRGAFGEATLYRRTEDDSLVMVWKEVDLTLSEKERRDALNEIVILALQHDNI 111
QY 64 VAFNSFOENGRFLFVMEYCDGDLMKRINRORGVLFSDDQILGWFWQVSLGLKHIDRK 123
DB 112 IAYYHFMONTLLILEYCNNGNLYDKLRQDKLFEEVMVWVLFQIVSAVSCIHKAG 171
QY 124 ILHRDIKAQNIPLSKNGMVAKLGFAGIARVLNNSMELARTCIGTPYLSPEICQNKPYNN 183
DB 172 ILHRDIKTINIPLTKANLI-KLGDYGLAKLNSEYSMAETLVGTVPYMSPELCQGVKNF 230
QY 184 KTDIWSLGCVLVELCTLKHPPFEGNNLQOLVLKICQAHFA--PISPGFSRELHSLISQLFQ 241
DB 231 KSDIWAAGCVIFELLTLTKRTFDATNPLNLCVQIGIRAMEVDSSQYLSLELIQMVHSCLD 290
QY 242 VSPRDRPSINSILKRPFLNIPKYLTPETVIOEFSHMLICRAGAPASRHAGKVQCKI 301
DB 291 QDPEQRTADELDRLRK-----RRREMEEK-----VTLNAPTKRPSRSTVTEAPI 339
QY 302 QKVRFR-----GKCPPR 313
DB 340 AVTSTRTSEVYVWGGGKSTPQ 360

RESULT 13
US-09-544-794-2
Sequence 2, Application US/09544794
Patent No. 6541232
GENERAL INFORMATION:
APPLICANT: Sims, John E.
APPLICANT: Virca, G. Duke
APPLICANT: Bird, Timothy A.
APPLICANT: Anderson, Dirk M.
TITLE OF INVENTION: Polypeptides Having Kinase Activity
FILE REFERENCE: 2005-B
CURRENT APPLICATION NUMBER: US/09/544,794
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 08/870,529
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/059,979
PRIOR FILING DATE: 1996-06-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 979
TYPE: PRT
ORGANISM: Homo sapiens
US-09-544-794-2

Query Match 15.8%; Score 538.5; DB 4; Length 979;
Best Local Similarity 36.1%; Pred. No. 1.1e-35;
Matches 116; Conservative 61; Mismatches 121; Indels 23; Gaps 5;

QY 4 YDVIKAIQGGAFKAYLAKGSDSKHCIVKINFEKMPIOQEASKEVILLESKHPNI 63

DB 52 YPIRVLGRGAFGEATLYRRTEDDSLVMVWKEVDLTLSEKERRDALNEIVILALQHDNI 111
QY 64 VAFNSFOENGRFLFVMEYCDGDLMKRINRORGVLFSDDQILGWFWQVSLGLKHIDRK 123
DB 112 IAYYHFMONTLLILEYCNNGNLYDKLRQDKLFEEVMVWVLFQIVSAVSCIHKAG 171
QY 124 ILHRDIKAQNIPLSKNGMVAKLGFAGIARVLNNSMELARTCIGTPYLSPEICQNKPYNN 183
DB 172 ILHRDIKTINIPLTKANLI-KLGDYGLAKLNSEYSMAETLVGTVPYMSPELCQGVKNF 230
QY 184 KTDIWSLGCVLVELCTLKHPPFEGNNLQOLVLKICQAHFA--PISPGFSRELHSLISQLFQ 241
DB 231 KSDIWAAGCVIFELLTLTKRTFDATNPLNLCVQIGIRAMEVDSSQYLSLELIQMVHSCLD 290
QY 242 VSPRDRPSINSILKRPFLNIPKYLTPETVIOEFSHMLICRAGAPASRHAGKVQCKI 301
DB 291 QDPEQRTADELDRLRK-----RRREMEEK-----VTLNAPTKRPSRSTVTEAPI 339
QY 302 QKVRFR-----GKCPPR 313
DB 340 AVTSTRTSEVYVWGGGKSTPQ 360

RESULT 14
US-09-167-206-2
Sequence 2, Application US/09167206A
Patent No. 6476193
GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Schulz, Vincent P.
APPLICANT: Yang, Meija
TITLE OF INVENTION: Nlk1 PROTEIN AND Nlk1 PROTEIN COMPLEXES
FILE REFERENCE: 15966-521 Nlk1 protein complexes
CURRENT APPLICATION NUMBER: US/09/167,206A
CURRENT FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 445
TYPE: PRT
ORGANISM: Homo sapiens
US-09-167-206-2

Query Match 15.7%; Score 535.5; DB 4; Length 445;
Best Local Similarity 29.7%; Pred. No. 6.8e-36;
Matches 140; Conservative 89; Mismatches 167; Indels 75; Gaps 13;

QY 2 DKYDVIKAIQGGAFKAYLAKGSDSKHCIVKINFEKMPIOQEASKEVILLESKHP 61
DB 6 EDYEVLTIGTGSYGRQKIRRSKSDGKILVWKELDYGSMTAEKQMLVSEVNLRELKHP 65
QY 62 NIYAFNSF--QENGRFLFVMEYCDGDLMKRI---NRORGVLFSDDQILGWFWQVSLGL 116
DB 66 NIVRYDRIIDRTNTTLIVIMEYCEGDGLASVTIKTKERQYL-DEEFLVRVMTQTJLAL 124
QY 117 KHIHDRK-----ILHRDIKAQNIPLSKNGMVAKLGFAGIARVLNNSMELARTCIGTPY 171
DB 125 KCHRRSDGGHTVLRDLKPAVFLDGKQNV-KLGFGLARILNHDTSFAKTFVGTPIYM 183
QY 172 SPEICQNKPYNNKTDIWSLGCVLVELCTLKHPPFEGNNLQOLVLKICQAHFAPISPGFSRE 231
DB 184 SPEQMNSYNEKSDIWSLGLLIELCALMPPTAFSQKELAGIKREGFRRIPIYYSDE 243
QY 232 LHSLSISQLFQVSPRDRPSINSILKRPFLNIPKYLTPETVIOEFSHMLICRA---GAP- 287
DB 244 LNEIITRLNLKDYHRPSVEILENPLIADL-----VADEQRNLERRGRQLGEP 294
QY 288 ASRHAGKVQCKIQKVRFGKCPPRSRISVPIKRNAILHNRWPPAGAKQ----- 339
DB 295 KSDSSPVLSELKKEIQLQ-----ERERALKARBERLEKQECLELCVRLA 341
QY 340 -----ARSTKMERPIAAVCGHYDYVQAQDLMLRRRAHKPSYHPIPQENTGV 389

Job time : 43 secs

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Db 342 EDKLARAENLLKNSLLKRFSLASNPPELLNLPSSVKKVH---FSGESKENI---- 394
Qy 390 YGQETHRGPSQWPAEYLOKFEAQO-----YKLKVEKQLGR 428
Db 395 MRSENSESQTSKCKDLKRLHAAQRAQALSDIEKNYOLKSRQILGMR 445

RESULT 15
US-09-538-092-1181
; Sequence 1181, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratPatSeqformatter Version 0.9
; SEQ ID NO 1181
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)-(0)
; OTHER INFORMATION: Polypeptide Accession Number P51955
US-09-538-092-1181
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Query Match 15.7%; Score 535.5; DB 4; Length 445;
Best Local Similarity 29.7%; Pred. No. 6.8e-36;
Matches 140; Conservative 89; Mismatches 167; Indels 75; Gaps 13;

Qy 2 DKYDVIKAIAGGAFKAYLAKGSDSKHCYVKEINFEKMPIOBEKSKKEVILLKXKHP 61
Db 6 EDYEVLYTIGTGYGRCQKIRRSKDGKILYMKELDYGMTAEKQMLVSEVNLRELKHP 65
Qy 62 NIVAFNSF--QENGRFIWVEYCDGDLMKRI---NRQGVLFSDQILGNFVQISLGL 116
Db 66 NIVRYDRIIDRTNTIYIWEYCEGDLASVITKTKERQYL-DEEFVLRVMTQLTAL 124
Qy 117 KHIHDRK-----ILHRDIKQNIPLSKNGMVAKLGDGFIARVLNNSMELARTCIGPIYL 171
Db 125 KCHRRSDGGHTVLHRLDKPANVFLDGQNV-KLGDGFLARILNHDTSFAKTFVGTPTYM 183
Qy 172 SPEICQKNPNKNTDIWSLGVLYELCTLKHPPPEGNNLQOLVLCIQAHPAPISPGFSRE 231
Db 184 SPEQNMMSVNEKSDIWSLGLYELCALMPPTAFSQKELAGKIRGKFRIPYRISDE 243
Qy 232 LHSLSIQLFQVSPRDRPSINSILKRPFLNIPKYLTPEVIOEFSHMLICRA---GAP- 287
Db 244 LNEIITRLMLKDYHRPSVEILENPLIADL-----VADEQRNLERRGRQLGEPE 294
Qy 288 ASRHAGKVQCKIQKVRFRGKCPFRSISVPIKRNAILHRENEWPPAGAK----- 339
Db 295 KSQDSSPVLSELKLEIQLQ-----ERERALKAREERLEQKEQLCVTERLA 341
Qy 340 -----ARSIKMIERPKIAVCHDYDYVAQLDMLRRRAHKPSYHPIQENTGVED 389
Db 342 EDKLARAENLLKNSLLKRFSLASNPPELLNLPSSVKKVH---FSGESKENI---- 394
Qy 390 YGQETHRGPSQWPAEYLOKFEAQO-----YKLKVEKQLGR 428
Db 395 MRSENSESQTSKCKDLKRLHAAQRAQALSDIEKNYOLKSRQILGMR 445
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OM protein - protein search, using sw model

Run on: November 12, 2004, 12:46:14 ; Search time 156 Seconds

(without alignments)
1471.710 Million cell updates/sec

Title: US-10-730-010-2

Perfect score: 3404

Sequence: 1 MDKYDVKAIGQAFGKAYL.....LCANDCSLKDWSEKEMELRT 640

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003s:*
7: Geneseqp2003Bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3404	100.0	640	6	ABG72000 Human ser
2	3081.5	90.5	683	5	Aau77928 Amino aci
3	3081.5	90.5	889	8	ADJ96637 Human Nim
4	2945	86.5	654	5	Aau77929 Amino aci
5	2715.5	79.8	649	4	Aau03545 Human pro
6	2610.5	76.7	631	6	ABP71710 Human NEK
7	2107.5	61.9	403	6	ABU54635 Human NOV
8	2102.5	61.8	399	6	ABU54634 Human NOV
9	1840.5	48.2	614	7	ADF44515 Mouse kin
10	1135.5	33.4	336	7	ADF44528 Mouse kin
11	1108.5	32.6	544	6	ABP96073 Human pro
12	1086	31.9	1242	4	AAM39210 Human pol
13	1086	31.9	1242	6	AAOI6440 Human ser
14	1078	31.7	774	6	AAO26613 Serine/th
15	1078	31.7	774	6	ABP71711 NEK-like
16	1078	31.7	774	6	AAOI6441 Human ser
17	1078	31.7	774	6	ABP7691 Amino aci
18	1072	31.5	1286	8	ADJ96638 Human Nim
19	1060	31.1	1214	4	AAU07102 Human nov
20	1056	31.0	1214	4	AAM39211 Human pol
21	1056	31.0	1214	6	ABU08113 Human kin
22	928	27.3	632	5	ABP55160 Ser/Thr/T
23	820.5	24.1	506	6	ABU54631 Human NOV
24	820.5	24.1	506	6	ADH42547 Novel hum
25	815.5	24.0	345	3	AAY76753 Human pro

26	815.5	24.0	345	4	AAE06211 Human pro
27	815.5	24.0	345	5	ABB84438 Human pro
28	814	23.9	461	8	ADI40836 Human kin
29	812	23.9	425	6	ABU54633 Human NOV
30	812	23.9	425	8	ADH42551 Novel hum
31	812	23.9	489	6	ABU54632 Human NOV
32	812	23.9	489	8	ADH42549 Novel hum
33	810.5	23.8	506	4	AAM78344 Human pro
34	810.5	23.8	506	5	ABP60668 Human ser
35	810.5	23.8	506	8	ADJ96639 Human Nim
36	808.5	23.8	506	5	AAE24136 Human kin
37	808	23.7	507	6	ABP97688 Amino aci
38	806.5	23.7	527	4	AAM79328 Human pro
39	806.5	23.7	527	5	ABB97224 Novel hum
40	805.5	23.7	511	6	ABP71712 NEK-like
41	805.5	23.7	511	6	ABP97690 Amino aci
42	804.5	23.6	546	6	ABP96072 Human pro
43	802	23.6	510	8	ADMI6429 Human kin
44	800	23.5	489	7	ADC93067 Human KPP
45	791.5	23.3	489	8	ADH42553 Novel hum

ALIGNMENTS

RESULT 1
ABG72000
ID ABG72000 standard; protein; 640 AA..

AC ABG72000;

XX 04-FEB-2003 (first entry)

XX Human serine/threonine kinase.

XX Human; enzyme; serine/threonine kinase; lung carcinoma; chromosome 13.

XX Homo sapiens.

XX WO200281727-A2.

XX PD 17-OCT-2002.

XX PF 02-APR-2002; 2002WO-US010156.

XX PR 03-APR-2001; 2001US-00824583.

XX PR 05-JUN-2001; 2001US-00873404.

XX (PEKE) PE CORP NY.

XX Webster M, Yan C, Di Francesco V, Beasley EM;

XX WPI; 2003-058562/05.

XX N-PSDB; ABS57149, ABS57150.

XX Novel human kinase protein expressed in lung carcinoma and placenta is useful to diagnose and treat diseases and disorders associated with expression or activity of the protein.

XX Claim 1; Fig 2A; 101pp; English.

XX The invention relates to an isolated human kinase peptide of the serine/threonine, an allelic variant or orthologue, and encoded by a nucleic acid that hybridises under stringent conditions with the cDNA and gene sequences appearing as ABS57149 and ABS57150, or a fragment comprising at least 10 contiguous amino acids. Also included are an antibody that selectively binds to the kinase, a gene chip comprising the nucleic acids, a transgenic non human animal comprising the nucleic acids, a nucleic acid vector comprising the nucleic acids, a host cell containing the vector and expressing the kinase, identifying a modulator/binding agent of the kinase (comprising contacting the peptide with an agent and determining if the agent has modulated function, expression or activity of the peptide or formed a complex with it), The

CC molecules of the invention are useful to diagnose and treat a disorder
 CC characterised by aberrant expression of the protein (e.g. lung
 CC carcinoma). Agents which modulate the function or activity of the protein
 CC are useful to treat diseases or disorders mediated by human kinase
 CC protein. The gene for encoding the novel kinase is located on chromosome
 CC 13. The present sequence represents the novel human kinase
 XX
 XX Sequence 640 AA;

Query Match 100.0%; Score 3404; DB 6; Length 640;
 Best Local Similarity 100.0%; Pred. No. 1.1e-269;
 Matches 640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKVDVIAIGGAGFGKAYLAKGSDSKHCIVKINFEKMPIQKEASKKEVILEKMKH 60
 DB 1 MDKVDVIAIGGAGFGKAYLAKGSDSKHCIVKINFEKMPIQKEASKKEVILEKMKH 60
 QY 61 PNIVAFNSFOENGRFLFTVMEYCDGGDLMKRINRQGVLFSEDOILGWFWQISLGLKHIH 120
 DB 61 PNIVAFNSFOENGRFLFTVMEYCDGGDLMKRINRQGVLFSEDOILGWFWQISLGLKHIH 120
 QY 121 DRKILHRDIKAQNIPLSKNGMVAKLGDGFIARVLNNSMELARTICGTPPYLSPEICQNK 180
 DB 121 DRKILHRDIKAQNIPLSKNGMVAKLGDGFIARVLNNSMELARTICGTPPYLSPEICQNK 180
 QY 181 YNNKTDIWSLGCVLVELCTLKHPPFEGNLLQOLVLIQAHFAPISPGFSRELHSLISOLF 240
 DB 181 YNNKTDIWSLGCVLVELCTLKHPPFEGNLLQOLVLIQAHFAPISPGFSRELHSLISOLF 240
 QY 241 QVSPDRPSINSILKRPFLNLI PKYLTPEVIOEFSHMLICRAGAPASHAGKVQKCK 300
 DB 241 QVSPDRPSINSILKRPFLNLI PKYLTPEVIOEFSHMLICRAGAPASHAGKVQKCK 300
 QY 301 IQKVFRCCKPRSRISVPIKRNAILHRNWRPAGAKARSIKMIERPKIAAVCGHYD 360
 DB 301 IQKVFRCCKPRSRISVPIKRNAILHRNWRPAGAKARSIKMIERPKIAAVCGHYD 360
 QY 361 YQAQLDMLRRRAHKPSYHIPQENTGVEDYQGETRHGSPSQWPAEYLQKFEAQYK 420
 DB 361 YQAQLDMLRRRAHKPSYHIPQENTGVEDYQGETRHGSPSQWPAEYLQKFEAQYK 420
 QY 421 VEKQLGLRPSAEPNQRQLRNGEPPRQELPFRNEMKEQYWKQLEERQOYLND 480
 DB 421 VEKQLGLRPSAEPNQRQLRNGEPPRQELPFRNEMKEQYWKQLEERQOYLND 480
 QY 481 MKEIRKMGREPDIEKDLQMRLONTKESKNPQKYKAKGVKFEINLDCISDENILQ 540
 DB 481 MKEIRKMGREPDIEKDLQMRLONTKESKNPQKYKAKGVKFEINLDCISDENILQ 540
 QY 541 EEEAMDIPNETLTPEDGMKFEYCVKEHGDYTDKAFELKHCPEAAFTLWLSFLEY 600
 DB 541 EEEAMDIPNETLTPEDGMKFEYCVKEHGDYTDKAFELKHCPEAAFTLWLSFLEY 600
 QY 601 SLPHFLLEKSPFSLHLEDLLCANDCSLKDWSEKEMELRT 640
 DB 601 SLPHFLLEKSPFSLHLEDLLCANDCSLKDWSEKEMELRT 640

RESULT 2
 AAU77928
 ID AAU77928 standard; protein; 683 AA.
 AC AAU77928;
 XX
 XX
 DT 18-JUN-2002 (first entry)
 XX Amino acid sequence for novel human kinase protein #1.
 DE
 DE
 KW Novel human protein; NHP; serine-threonine kinase; brain;
 KW calcium/calmodulin-dependent kinase; myosin light chain kinase;
 KW biological disorder; spleen; placenta; chromosome 6; enzyme.
 XX
 XX Homo sapiens.

XX WO200218555-A2.
 PN 07-MAR-2002.
 XX 28-AUG-2001; 2001WO-US026775.
 XX 31-AUG-2000; 2000US-0229280P.
 XX (LEXI-) LEXICON GENETICS INC.
 PA Friddle CJ, Hilbun B, Nepomnichy B, Hu Y;
 PI WPI: 2002-292200/33.
 DR N-PSDB; ABK12424.
 XX Novel polynucleotide encoding novel human protein sharing structural
 PT similarity with animal kinases e.g. serine-threonine, calcium/calmodulin-
 dependent, and myosin light chain kinases, useful as probes and primers.
 XX Claim 1; Page 38-39; 46pp; English.
 CC The present invention relates to the isolation of novel human proteins
 CC (NHPs) and the polynucleotide sequences encoding them. The NHPs of the
 CC invention are kinase proteins and share structural similarity to serine-
 CC threonine, calcium/calmodulin-dependent, and myosin light chain kinases.
 CC The sequences of the invention are useful for treating biological
 CC disorders. The polynucleotide sequences encoding the kinase proteins can
 CC be used as primers and probes. The sequences are also useful for
 CC identifying mutations associated with a particular disease and also in a
 CC prognostic or diagnostic assay. The present sequence represents human
 CC protein kinase #1 which is expressed in a broad range of human tissues
 CC such as brain, spleen, and placenta. The gene encoding protein kinase #1
 CC is located on chromosome 6
 XX Sequence 683 AA;

Query Match 90.5%; Score 3081.5; DB 5; Length 683;
 Best Local Similarity 94.1%; Pred. No. 3.1e-243;
 Matches 585; Conservative 2; Mismatches 4; Indels 31; Gaps 1;

QY 1 MDKVDVIAIGGAGFGKAYLAKGSDSKHCIVKINFEKMPIQKEASKKEVILEKMKH 60
 DB 1 MDKVDVIAIGGAGFGKAYLAKGSDSKHCIVKINFEKMPIQKEASKKEVILEKMKH 60
 QY 61 PNIVAFNSFOENGRFLFTVMEYCDGGDLMKRINRQGVLFSEDOILGWFWQISLGLKHIH 120
 DB 61 PNIVAFNSFOENGRFLFTVMEYCDGGDLMKRINRQGVLFSEDOILGWFWQISLGLKHIH 120
 QY 121 DRKILHRDIKAQNIPLSKNGMVAKLGDGFIARVLNNSMELARTICGTPPYLSPEICQNK 180
 DB 121 DRKILHRDIKAQNIPLSKNGMVAKLGDGFIARVLNNSMELARTICGTPPYLSPEICQNK 180
 QY 181 YNNKTDIWSLGCVLVELCTLKHPPFEGNLLQOLVLIQAHFAPISPGFSRELHSLISOLF 240
 DB 181 YNNKTDIWSLGCVLVELCTLKHPPFEGNLLQOLVLIQAHFAPISPGFSRELHSLISOLF 240
 QY 241 QVSPDRPSINSILKRPFLNLI PKYLTPEVIOEFSHMLICRAGAPASHAGKVQKCK 300
 DB 241 QVSPDRPSINSILKRPFLNLI PKYLTPEVIOEFSHMLICRAGAPASHAGKVQKCK 300
 QY 301 IQKVFRCCKPRSRISVPIKRNAILHRNWRPAGAKARSIKMIERPKIAAVCGHYD 360
 DB 301 IQKVFRCCKPRSRISVPIKRNAILHRNWRPAGAKARSIKMIERPKIAAVCGHYD 360
 QY 361 YQAQLDMLRRRAHKPSYHIPQENTGVEDYQGETRHGSPSQWPAEYLQKFEAQYK 420
 DB 361 YQAQLDMLRRRAHKPSYHIPQENTGVEDYQGETRHGSPSQWPAEYLQKFEAQYK 420
 QY 421 VEKQLGLRPSAEPNQRQLRNGEPPRQELPFRNEMKEQYWKQLEERQOYLND 480
 DB 421 VEKQLGLRPSAEPNQRQLRNGEPPRQELPFRNEMKEQYWKQLEERQOYLND 480

QY 481 MKEIRKMGREPE-----DIEKDLKQRLQNTKE 509
DB 481 MKEIRKMGREPEENSKISHKTYLVKKSNNLPVHQDASEGEAPVQDIEKDLKQRLQNTKE 540
QY 510 SKNPEQYKAKGVKFEINLDCISDENILOBEEAMDIPNETLTTFEDGMKFEYECVKEH 569
DB 541 SKNPEQYKAKGVKFEINLDCISDENILOBEEAMDIPNETLTTFEDGMKFEYECVKEH 600
QY 570 GDYTDKAFKHLHCPAAFTLT 591
DB 601 GDYTDKAFKHLHCPAGFSTQT 622

RESULT 3
ID ADJ96637 standard; protein; 889 AA.
AC ADJ96637;
XX
DT 06-MAY-2004 (first entry)
DE Human Nim-A related protein kinase NEK5 protein SeqID 94.
XX
KW kinase; human; tyrosine protein kinase; serine/threonine protein kinase;
KW PTX; STK; gene therapy; cancer; immune-related disease;
KW cardiovascular disease; brain; neuronal associated disease; metabolic;
KW inflammatory disorder; cytostatic; neuroprotective; immunomodulator;
KW antiinflammatory; enzyme; Nim-A related protein kinase; NEK5.
XX
OS Homo sapiens.
OS 56.
XX
XX WO2004006838-A2.
XX
XX 22-JAN-2004.
XX
XX 15-JUL-2003; 2003WO-US021730.
XX
XX 15-JUL-2002; 2002US-0395632P.
XX
XX (SUGS-) SUGEN INC.
XX
XX Whyte D, Manning G, Caenepeel S;
XX
XX WPI; 2004-122753/12.
XX
XX N-PSDB; ADJ96571.
XX
XX New nucleic acid molecule encoding a kinase polypeptide, useful for
XX PT preparing a composition for treating diseases or disorders, e.g., cancer,
XX PT or neurological, immunological or inflammatory disorders.
XX
XX Claim 1; SEQ ID NO 94; 366pp; English.

CC This invention relates to a novel isolated, enriched or purified nucleic
CC acid molecule that encodes a kinase polypeptide. Specifically, it relates
CC to human tyrosine and serine/threonine protein kinases (PTK's and STK's),
CC as well as protein kinase-like enzymes. The present invention describes
CC screening methods to identify agonists, antagonists and antibodies that
CC can be used to modulate the activity or function of the mammalian kinase
CC enzymes. As such, these compositions can be used for gene therapy
CC purposes to treat diseases or disorders including cancer, immune-related
CC diseases, cardiovascular disease, brain or neuronal associated disease,
CC metabolic and inflammatory disorders. Accordingly, they exhibit
CC cytostatic, neuroprotective, immunomodulator and antiinflammatory
CC activities. This polypeptide sequence is a human kinase protein sequence
CC of the invention.

XX
XX
XX Sequence 889 AA;

Query Match 90.5%; Score 3081.5; DB 8; Length 889;
Best Local Similarity 94.1%; Pred. No. 4.4e-243;
Matches 585; Conservative 2; Mismatches 4; Indels 31; Gaps 1;

QY 1 MDKYDVIIKAIQGOAFGKAYLAKGKSDSKHCYVIKEINFEKMPIQEKESKKEVILEKMKH 60
DB 58 MDKYDVIIKAIQGOAFGKAYLAKGKSDSKHCYVIKEINFEKMPIQEKESKKEVILEKMKH 117
QY 61 PNIVAFNSFOENGRLFIWMEYCDGDLMKRINRQGVLPSEDIILGWFOISLGLKHH 120
DB 118 PNIVAFNSFOENGRLFIWMEYCDGDLMKRINRQGVLPSEDIILGWFOISLGLKHH 177
QY 121 DRKILHRDIIKAQNIIFLSKNGWAKLGDGFIARVLNNSMELARTICGTPPYLSPEICQK 180
DB 178 DRKILHRDIIKAQNIIFLSKNGWAKLGDGFIARVLNNSMELARTICGTPPYLSPEICQK 237
QY 181 YNNKTDIWSLGCVLVELCTLKHPEGNLQVLKICQAHFAPISPGFSELHSLISQLF 240
DB 238 YNNKTDIWSLGCVLVELCTLKHPEGNLQVLKICQAHFAPISPGFSELHSLISQLF 297
QY 241 QVSPDRPSINSILKRPFLNLPKYLTPVIQEEFSHMLICRAGAPASHAGKVQCK 300
DB 298 QVSPDRPSINSILKRPFLNLPKYLTPVIQEEFSHMLICRAGAPASHAGKVQCK 357
QY 301 IQKVRFGKCPPRSISVPIKRNAILHRNEWPPAGAKARSIMIERPKIAAVCGHYD 360
DB 358 IQKVRFGKCPPRSISVPIKRNAILHRNEWPPAGAKARSIMIERPKIAAVCGHYD 417
QY 361 YYAQLDMLRRRAHKPSYHPPIQENTGVEDYQOETHGSPSPQPAEYLQKFEAQOYK 420
DB 418 YYAQLDMLRRRAHKPSYHPPIQENTGVEDYQOETHGSPSPQPAEYLQKFEAQOYK 477
QY 421 VEKQLGLRPSAEPNNYQRELRSNGEPRFQELPFRKNEMKEQYWKOLEEIRQQYLND 480
DB 478 VEKQLGLRPSAEPNNYQRELRSNGEPRFQELPFRKNEMKEQYWKOLEEIRQQYLND 537
QY 481 MKEIRKMGREPE-----DIEKDLKQRLQNTKE 509
DB 538 MKEIRKMGREPEENSKISHKTYLVKKSNNLPVHQDASEGEAPVQDIEKDLKQRLQNTKE 597
QY 510 SKNPEQYKAKGVKFEINLDCISDENILOBEEAMDIPNETLTTFEDGMKFEYECVKEH 569
DB 598 SKNPEQYKAKGVKFEINLDCISDENILOBEEAMDIPNETLTTFEDGMKFEYECVKEH 657
QY 570 GDYTDKAFKHLHCPAAFTLT 591
DB 658 GDYTDKAFKHLHCPAGFSTQT 679

RESULT 4

AAU77929
ID AAU77929 standard; protein; 654 AA.
XX
AC AAU77929;

DT 18-JUN-2002 (first entry)

XX Amino acid sequence for novel human kinase protein #2.
XX
XX Novel human protein; NHP; serine-threonine kinase; brain;
XX calcium/calmodulin-dependent kinase; myosin light chain kinase;
XX biological disorder; spleen; placenta chromosome 6; enzyme.

XX Homo sapiens.

XX WO200218555-A2.

XX 07-MAR-2002.

XX 28-AUG-2001; 2001WO-US026776.

XX 31-AUG-2000; 2000US-0229280P.

XX (LEXI-) LEXICON GENETICS INC.

XX Friddle CJ, Hilbun E, Nepomnichy B, Hu Y;

DR WPI; 2002-292200/33.

DR N-PSDB; ABK12425.

XX Novel polynucleotide encoding novel human protein sharing structural
PT similarity with animal kinases e.g. serine-threonine, calcium/calmodulin-
PT dependent, and myosin light chain kinases, useful as probes and primers.
XX
XX
PS Claim 3; Page 40-41; 46pp; English.

XX The present invention relates to the isolation of novel human proteins
CC (NHPs) and the polynucleotide sequences encoding them. The NHPs of the
CC invention are kinase proteins and share structural similarity to serine-
CC threonine, calcium/calmodulin-dependent, and myosin light chain kinases.
CC The sequences of the invention are useful for treating biological
CC disorders. The polynucleotide sequences encoding the kinase proteins can
CC be used as primers and probes. The sequences are also useful for
CC identifying mutations associated with a particular disease and also in a
CC prognostic or diagnostic assay. The present sequence represents human
CC protein kinase #2 which is expressed in a broad range of human tissues
CC such as brain, spleen, and placenta. The gene encoding protein kinase #2
CC is located on chromosome 6
XX
SQ Sequence 654 AA;

Query Match 86.5%; Score 2945; DB 5; Length 654;

Best Local Similarity 94.3%; Pred. No. 4.4e-232;

Matches 564; Conservative 7; Mismatches 15; Indels 12; Gaps 4;

QY 1 MDKYDVIKAIQGGAFKAYLAKGSDSKHCVIKINFEKMPIQEKASKKEVILEKWKH 60
DB 1 MDKYDVIKAIQGGAFKAYLAKGSDSKHCVIKINFEKMPIQEKASKKEVILEKWKH 60
QY 61 PNIVAFNFSFQENGLFTWMEYCDGDLMKRINRQGVLFSEDOILGFWQISLGLKHII 120
DB 61 PNIVAFNFSFQENGLFTWMEYCDGDLMKRINRQGVLFSEDOILGFWQISLGLKHII 120
QY 121 DRKILHRDIKQNTIFLSKNGVAKLGFGIARVLNNSMELARTICIGTPYLSPEICQNK 180
DB 121 DRKILHRDIKQNTIFLSKNGVAKLGFGIARVLNNSMELARTICIGTPYLSPEICQNK 180
QY 181 YNNKTDIWSLGCVLVELCTLKHPEGNLQOLVLKI COAHFAPISPGFSRELHSLISOLF 240
DB 181 YNNKTDIWSLGCVLVELCTLKHPEGNLQOLVLKI COAHFAPISPGFSRELHSLISOLF 240
QY 241 QVSPDRPSINSILKRPENLIPKYLTPETVIOEFSHMLICRAGAPASHAGKVVQCK 300
DB 241 QVSPDRPSINSILKRPENLIPKYLTPETVIOEFSHMLICRAGAPASHAGKVVQCK 300
QY 301 IQKVRFGKCPFRSISVPIKRNAILHRNEWPPAGAKARSIMIERPKIAAVCGHYD 360
DB 301 IQKVRFGKCPFRSISVPIKRNAILHRNEWPPAGAKARSIMIERPKIAAVCGHYD 360
QY 361 YYAQLDMLRRRAHPSYHPIQENTVEDYQETRHGSPSPQPAEYLQKFAQYK 420
DB 361 YYAQLDMLRRRAHPSYHPIQENTVEDYQETRHGSPSPQPAEYLQKFAQYK 420
QY 421 VEKQLGLRPSAEPNRYQRLNSGEPFRQELPFRKNEMKEQYWKQLEE---IROQY 477
DB 421 VEKQLGLRPSAEPNRYQRLNSGEPFRQELPFRKNEMKEQYWKQLEE---IROQY 477
QY 478 L---NDMKIEIKNGREP-EDIEKDLQMLONTKESKNPEQKYAKGKVPKPEINDKCI 533
DB 481 LPVHQDASE-----GEAPVQDIEKDLQMLONTKESKNPEQKYAKGKVPKPEINDKCI 535
QY 534 SDENILQEEAMDPNETLTPEDCMKFEVCKEKGHDYTDKAFELHCPAEAFTEL 591
DB 536 SDENILQEEAMDPNETLTPEDCMKFEVCKEKGHDYTDKAFELHCPAEAFTEL 593

RESULT 5

ID AAU03545

XX AAU03545 standard; protein; 649 AA.

AAU03545;

XX 12-SEP-2001 (first entry)

XX Human protein kinase #45.

XX Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
KW metabolic disorder; immune related disease; neurological disorder;
KW neurodegenerative disorder; inflammatory disorder; infectious disease;
reproductive disorder.
XX Homo sapiens.

XX WO200138503-A2.

XX 31-MAY-2001.

XX 22-NOV-2000; 2000WO-US032085.

XX 24-NOV-1999; 99US-0167482P.

XX (SUGEN-) SUGEN INC.

XX Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;

XX Planagan P, Clary D;

XX WPI; 2001-343950/36.

XX N-PSDB; AAS06745.

XX Nucleic acids encoding human kinase polypeptides, useful for preventing
PT diagnosing and/or treating e.g. cancer, immune cardiovascular and
PT neuronal-associated diseases, and microbial infections.

XX Claim 7; Fig 2; 433pp; English.

XX AAU03501-AAU03557 represent novel human protein kinases #1-57. The novel
CC protein kinases have been identified as members of the tyrosine or
CC serine/threonine kinase (PTK and STK) families. The polynucleotides
CC encoding protein kinases and the polypeptides may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate kinase expression. For example, they may be used to treat
CC cancers (especially cancers of haematopoietic origin), cardiovascular
CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
CC immune related diseases (e.g. rheumatoid arthritis), neurological
CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
CC Additionally, polynucleotides encoding protein kinases may be used for
CC gene therapy and as DNA probes in diagnostic assays. The protein kinase
CC polypeptides may be used as antigens in the production of antibodies
CC against the protein kinases and in assays to identify modulators of
CC protein kinase expression and activity

XX Sequence 649 AA;

Query Match 79.8%; Score 2715.5; DB 4; Length 649;

Best Local Similarity 88.4%; Pred. No. 2.7e-213;

Matches 526; Conservative 10; Mismatches 26; Indels 33; Gaps 5;

QY 1 MDKYDVIKAIQGGAFKAYLAKGSDSKHCVIKINFEKMPIQEKASKKEVILEKWKH 60
DB 1 MDKYDVIKAIQGGAFKAYLAKGSDSKHCVIKINFEKMPIQEKASKKEVILEKWKH 60
QY 61 PNIVAFNFSFQENGLFTWMEYCDGDLMKRINRQGVLFSEDOILGFWQISLGLKHII 120
DB 61 PNIVAFNFSFQENGLFTWMEYCDGDLMKRINRQGVLFSEDOILGFWQISLGLKHII 120
QY 121 DRKILHRDIKQNTIFLSKNGVAKLGFGIARVLNNSMELARTICIGTPYLSPEICQNK 180
DB 121 DRKILHRDIKQNTIFLSKNGVAKLGFGIARVLNNSMELARTICIGTPYLSPEICQNK 180
QY 181 YNNKTDIWSLGCVLVELCTLKHPEGNLQOLVLKI COAHFAPISPGFSRELHSLISOLF 240

Db 181 YNNKTDIWSLGCVLVELCTLKHPFEGNNLQQLVLTICQAHFAPISPGFSRELHSLISQLF 240
 QY 241 QVSPDRPSINSILKRPFLNIPKYLTPDEVIOEE-----FSHMLICRAGAPASRHAGKV 296
 Db 241 QVSPDRPSINSILKRPFLNIPKYLTPDEVIOEE-----FSHMLICRAGAPASRHAGKV 296
 QY 297 QKCKIOKVRGKCPKPPRSISVPIKNNAILHRNWRPPAGAQAQAKSIRMIEPKIAAVCG 356
 Db 289 -----LTRV-FGRCEPLHACIMVFNK-----PSCFLQ-----IKMIEPKIAAVCG 331
 QY 357 HYDYVYQAQDLMLRRRAHKSYPHPIPOENTGVEDYQETRHGSPSQWPAEYLQKFEAQ 416
 Db 332 HYDYVYQAQDLMLRRRAHKSYPHPIPOENTGVEDYQETRHGSPSQWPAEYLQKFEAQ 391
 QY 417 YKLKVEKQLGLRPSAEPNQRQLRSNGEPRFOELPFRKNENKEQYWKQLEIRQQ 476
 Db 392 YKLKVEKQLGLRPSAEPNQRQLRSNGEPRFOELPFRKNENKEQYWKQLEIRQQ 451
 QY 477 YLNDMKEIRKMGREPEDEKOLKQMLQNTKESKNPEQYKAKGVKFEINLDCISDE 536
 Db 452 YLNDMKEIRKMGREPEDEKOLKQMLQNTKESKNPEQYKAKGVKFEINLDCISDE 511
 QY 537 NILQEEBAMDIPNETLTFEDGMKFEYECVKEHGDYTDKAFKELHCPPEAAFTLT 591
 Db 512 NILQEEBAMDIPNETLTFEDGMKFEYECVKEHGDYTDKAFKELHCPPEAGFSTQT 566

RESULT 6

ID ABP71710
 AC ABP71710 standard; protein; 631 AA.

XX ABP71710;

DT 17-APR-2003 (first entry)

DE Human NEK-like serine/threonine protein kinase # SEQ ID 2.

XX Human; NEK-like serine/threonine protein kinase; cytostatic; cardiant;
 KW antiinflammatory; nectropic; neuroprotective; cancer; colon cancer;
 KW cardiovascular disorder; diabetes; COPD; CNS disorder.

XX Homo sapiens.

XX WO2003000903-A2.

XX 03-JAN-2003.

XX 24-JUN-2002; 2002WO-BP006948.

XX 25-JUN-2001; 2001US-0300068P.

PR 07-DEC-2001; 2001US-0336704P.

XX (FARB) BAYER AG.

XX Xiao Y;

XX WPI; 2003-184051/18.

DR N-PSDB; ABZ59716.

XX New polynucleotide encoding a NEK-like serine/threonine kinase

PT Polypeptide useful for treating diseases associated with kinase

PT dysfunction, e.g. cardiovascular disorders, cancer such as colon cancer,

PT diabetes and CNS disorders.

XX Claim 1 a ii; Fig 2; 149pp; English.

XX The invention relates to a newly isolated polynucleotide encoding an NEK-
 CC like serine/threonine protein kinase. The activity of the polynucleotide
 CC and polypeptide of the invention may be described as cytostatic,
 CC cardiant, antiinflammatory, nectropic and neuroprotective. The expression
 CC vector and reagent of the invention are useful for the preparation of a
 CC medicament for modulating the activity of an NEK-like serine/threonine
 CC kinase in a disease, such as cancer (e.g. colon cancer), cardiovascular

CC disorder, diabetes, COPD or CNS disorder. The polypeptides may also be
 CC used to identify compounds which may act as activators or inhibitors at
 CC the enzyme's active site, to raise specific antibodies which can block
 CC the enzyme and effectively reduce its activity, as a bait protein in a
 CC two-hybrid or three-hybrid assay to identify other proteins which bind to
 CC or interact with the human NEK-like serine/threonine kinase polypeptide
 CC and modulate its activity, and for the immunisation of mammals. The
 CC current sequence represents the human NEK-like serine/threonine protein
 CC kinase of the invention

XX SQ Sequence 631 AA;

Query Match 76.7%; Score 2610.5; DB 6; Length 631;

Best Local Similarity 85.8%; Pred. No. 1e-204;

Matches 512; Conservative 4; Mismatches 26; Indels 55; Gaps 5;

QY 1 MDKYDVYKALGQAFGKAYLAKGSKHCVKEINPEKMPIQEKASKKEVILEKMKH 60

Db 1 MDKYDVYKALGQAFGKAYLAKGSKHCVKEINPEKMPIQEKASKKEVILEKMKH 60

QY 61 PNIVAFNSFOENGRLEFVMEYCDGGDLMKRINRQGVLFSEDIQILGWFOISLGLKHH 120

Db 61 PNIVAFNSFOENGRLEFVMEYCDGGDLMKRINRQGVLFSEDIQILGWFOISLGLKHH 120

QY 121 DRKTLHEDIKAQNTFLSKNGWAKLGDGFIARVNNNSMELARTCIGTPYVLSPEICQKP 180

Db 121 DRKTLHEDIKAQNTFLSKNGWAKLGDGFIARVNNNSMELARTCIGTPYVLSPEICQKP 180

QY 181 YNNKTDIWSLGCVLVELCTLKHPPEGNNLQQLVLTICQAHFAPISPGFSRELHSLISQLF 240

Db 181 YNNKTDIWSLGCVLVELCTLKHPPEGNNLQQLVLTICQAHFAPISPGFSRELHSLISQLF 240

QY 241 QVSPDRPSINSILKRPFLNIPKYLTPDEVIOEFSHMLICRAGAPASRHAGKVQKCK 300

Db 241 QVSPDRPSINSILKRPFLNIPKYLTPDEVIOEFSHMLICRAGAPASRHAGKVQKCK 300

QY 301 IQKVRPCKGKPPSRISVP-----IKRNAILHRNWRPPAGAQAQAK--SIKMIERPKIAAV 354

Db 298 ----RHGT-----VRSGLSRPWAALLRLCRLOPIRLISQAAVECLRLFOIKMIERPKIAAV 350

QY 355 CGHYDYVYQAQDLMLRRRAHKSYPHPIPOENTGVEDYQETRHGSPSQWPAEYLQKFEA 414

Db 351 CGHYDYVYQAQDLMLRRRAHKSYPHPIPOENTGVEDYQETRHGSPSQWPAEYLQKFEA 410

QY 415 QQYKLKVEKQLGLRPPSAEPNQRQLRSNGEPRFOELPFRKNENKEQYWKQLEIR 474

Db 411 QQYKLKVEKQL-----EYWKQLEIR 431

QY 475 QQYLDNMYEIRKMGREPEDEKDLKOMRLQNTKESKNPEQYKAKGVKFEINLDCIS 534

Db 432 QQYHNDMKEIRKMGREPEDEKDLKOMRLQNTKESKNPEQYKAKGVKFEINLDCIS 491

QY 535 DENILOBEEAMDIPNETLTFEDGMKFEYECVKEHGDYTDKAFKELHCPPEAAFTLT 591

Db 492 DENILOBEEAMDIPNETLTFEDGMKFEYECVKEHGDYTDKAFKELHCPPEAGFSTQT 548

RESULT 7

ABU54635

ID ABU54635 standard; protein; 403 AA.

XX ABU54635;

XX 03-JUN-2003 (first entry)

XX Human NOVX polypeptide #94.

XX Human; NOVX; metabolic disorder; cardiomyopathy; diabetes; ASD;
 KW hypertension; congenital heart defect; aortic stenosis; valve disease;
 KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;
 KW pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD;
 KW tuberculous sclerosis; scleroderma; atherosclerosis; infectious disease;
 KW obesity; anorexia; neurodegenerative disorder; Alzheimer's disease;

KW Parkinson's disease; immune disorder; haematopoietic disorder;
 KW haemophilia; hypercoagulation; Crohn's disease; cancer.

XX Homo sapiens.

XX WO200281498-A2.

XX 17-OCT-2002.

XX 03-APR-2002; 2002WO-US010780.

XX 03-APR-2001; 2001US-0281086P.

XX 03-APR-2001; 2001US-0281136P.

XX 05-APR-2001; 2001US-0281863P.

XX 06-APR-2001; 2001US-0281906P.

XX 10-APR-2001; 2001US-0282930P.

XX 10-APR-2001; 2001US-0282930P.

XX 12-APR-2001; 2001US-0283512P.

XX 13-APR-2001; 2001US-0283710P.

XX 17-APR-2001; 2001US-0284234P.

XX 19-APR-2001; 2001US-0285325P.

XX 20-APR-2001; 2001US-0285381P.

XX 20-APR-2001; 2001US-0285609P.

XX 23-APR-2001; 2001US-0285748P.

XX 23-APR-2001; 2001US-0285890P.

XX 24-APR-2001; 2001US-0286068P.

XX 25-APR-2001; 2001US-0286292P.

XX 27-APR-2001; 2001US-0287213P.

XX 02-MAY-2001; 2001US-0288257P.

XX 29-MAY-2001; 2001US-0294164P.

XX 30-MAY-2001; 2001US-0294484P.

XX 18-JUN-2001; 2001US-0298952P.

XX 19-JUN-2001; 2001US-0299237P.

XX 19-JUN-2001; 2001US-0299276P.

XX 12-SEP-2001; 2001US-0318750P.

XX 25-SEP-2001; 2001US-0324800P.

XX 25-SEP-2001; 2001US-0324802P.

XX 17-SEP-2001; 2001US-0325684P.

XX 17-OCT-2001; 2001US-0330143P.

XX 14-NOV-2001; 2001US-0332131P.

XX 14-NOV-2001; 2001US-0332240P.

XX 14-NOV-2001; 2001US-0332779P.

XX 21-NOV-2001; 2001US-0332115P.

XX 04-DEC-2001; 2001US-0337621P.

XX 03-JAN-2002; 2002US-0345783P.

XX 16-JAN-2002; 2002US-0350251P.

XX 02-APR-2002; 2002US-00114270.

(CURA-) CURAGEN CORP.

Guo X, Kekuda R, Miller CE, Malvankar UM, Spytek KA;

Patturajan M, Liu X, Gusev VI, Li L, Vernet CAM, Zerhusen BD;

Gorman L, Shenoy SG, Pena CE, Smithson G, Burgess CE, Gerlach V;

Padigaru M, Shinkets RA, Gangoli EA, Taupier RJ, Casman SJ, Ji W;

Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ;

MacDougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA;

Ellerman K;

WPI; 2003-045858/04.

N-PSDB; ABX72263.

New isolated NOVX polypeptide useful for treating atherosclerosis,

metabolic disorders, diabetes, obesity, infectious disease, anorexia,

neurodegenerative disorders, Alzheimer's disease and cancer.

Claim 1; Page 292; 66pp; English.

The invention relates to human polypeptides, termed NOVX, and the

polynucleotides encoding them. The polypeptides and polynucleotides are

useful for diagnosing disease, and screening for potential therapeutic

agents. The sequences are useful for treating metabolic disorders,

cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic

CC stenosis, atrial septal defect (ASD), atrioventricular canal defect,
 CC ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular
 CC septal defect (VSD), valve diseases, tuberosus sclerosis, scleroderma,
 CC atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative
 CC disorders, Alzheimer's disease, Parkinson's disease, immune disorders,
 CC haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease
 CC and cancer. Sequences ABUS4542-ABUS4647 represent human NOVX polypeptides
 CC of the invention

XX Sequence 403 AA;

SQ Query Match 61.9%; Score 2107.5; DB 6; Length 403;

Best Local Similarity 98.8%; Pred. No. 9e-164;

Matches 398; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 MDKYDVIRKAIQGGAFKAYLAKGSDSKHCVIKKEINFEKMPIQEAKSKKEVILLKMKH 60

Db 1 MDKYDVIRKAIQGGAFKAYLAKGSDSKHCVIKKEINFEKMPIQEAKSKKEVILLKMKH 60

QY 61 PNIVAFNSFOENGRLFIWMEYCDGGDLMKGINRQGVLFSEDOILGFVQISLGLKHH 120

Db 61 PNIVAFNSFOENGRLFIWMEYCDGGDLMKGINRQGVLFSEDOILGFVQISLGLKHH 120

QY 121 DRKILHRDIKQNIPLSKNGMVAKLGDGFIARVLNNSMELARTCIGTPYILSPICQNK 180

Db 121 DRKILHRDIKQNIPLSKNGMVAKLGDGFIARVLNNSMELARTCIGTPYILSPICQNK 180

QY 181 YNKTDIWSLGLCVLYELCTLKHPPFEGNNLQQLVKICQAHFAPISPGFSRHLHLSQLF 240

Db 181 YNKTDIWSLGLCVLYELCTLKHPPFEGNNLQQLVKICQAHFAPISPGFSRHLHLSQLF 240

QY 241 QVSPDRPSINSILKPELENI PKYLTPEV IQEESHMLICRAGAPASHAGKVQKC 299

Db 241 QVSPDRPSINSILKPELENI PKYLTPEV IQEESHMLICRAGAPASHAGKVQKC 300

QY 300 KIQKVRFRGKCPPRSRSISVPIKRNAILHRENRWPPAGAKARSIKMIERPPIAAVCGHYD 359

Db 301 KIQKVRFRGKCPPRSRSISVPIKRNAILHRENRWPPAGAKARSIKMIERPPIAAVCGHYD 360

QY 360 YYYAQLDMLRRRAHPSYHPIPOENTGVEDYGOETRHGSPSQ 402

Db 361 YYYAQLDMLRRRAHPSYHPIPOENTGVEDYGOETRHGSPSQ 403

RESULT 8

ABUS4634

ID ABUS4634 standard; protein; 399 AA.

XX AC ABUS4634;

XX DT 03-JUN-2003 (first entry)

XX DE Human NOVX polypeptide #93.

XX KW Human; NOVX; metabolic disorder; cardiomyopathy; diabetes; ASD;

XX KW hypertension; congenital heart defect; aortic stenosis; valve disease;

XX KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;

XX KW pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD;

XX KW tuberosus sclerosis; scleroderma; atherosclerosis; infectious disease;

XX KW obesity; anorexia; neurodegenerative disorder; Alzheimer's disease;

XX KW Parkinson's disease; immune disorder; haematopoietic disorder;

XX KW haemophilia; hypercoagulation; Crohn's disease; cancer.

XX OS Homo sapiens.

XX PN WO200281498-A2.

XX PD 17-OCT-2002.

XX PF 03-APR-2002; 2002WO-US010780.

XX PR 03-APR-2001; 2001US-0281086P.

XX PR 03-APR-2001; 2001US-0281136P.

05-APR-2001; 2001US-0281863P.
 06-APR-2001; 2001US-0281906P.
 06-APR-2001; 2001US-0282020P.
 10-APR-2001; 2001US-0282930P.
 10-APR-2001; 2001US-0282934P.
 12-APR-2001; 2001US-028312P.
 13-APR-2001; 2001US-0283710P.
 17-APR-2001; 2001US-0284234P.
 19-APR-2001; 2001US-0285325P.
 20-APR-2001; 2001US-0285381P.
 20-APR-2001; 2001US-0285609P.
 23-APR-2001; 2001US-0285748P.
 23-APR-2001; 2001US-0285890P.
 24-APR-2001; 2001US-0286068P.
 25-APR-2001; 2001US-0286292P.
 27-APR-2001; 2001US-0287213P.
 02-MAY-2001; 2001US-0288257P.
 29-MAY-2001; 2001US-0294164P.
 30-MAY-2001; 2001US-0294484P.
 18-JUN-2001; 2001US-0296952P.
 19-JUN-2001; 2001US-0299237P.
 19-JUN-2001; 2001US-0299276P.
 12-SEP-2001; 2001US-0318750P.
 25-SEP-2001; 2001US-0324800P.
 25-SEP-2001; 2001US-0324802P.
 27-SEP-2001; 2001US-0325684P.
 17-OCT-2001; 2001US-0330143P.
 14-NOV-2001; 2001US-0332131P.
 14-NOV-2001; 2001US-0332240P.
 14-NOV-2001; 2001US-0332779P.
 21-NOV-2001; 2001US-0332115P.
 04-DEC-2001; 2001US-0337621P.
 03-JAN-2002; 2002US-0345783P.
 16-JAN-2002; 2002US-0350251P.
 02-APR-2002; 2002US-00114270.
 (CURA-) CURAGEN CORP.
 Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA;
 Patturajan M, Liu X, Gusev VT, Li L, Vernet CAM, Zethusen BD;
 Gorman L, Shenoy SG, Pena CE, Smithson G, Burgess CE, Gerlach V;
 Padigaru M, Shinkets RA, Gangolli EA, Taupier RJ, Casman SJ, Ji W;
 Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ;
 Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA;
 Ellerman K;
 WPI; 2003-046858/04.
 N-PSDB; ABX72262.
 New isolated NOVX polypeptide useful for treating atherosclerosis,
 metabolic disorders, diabetes, obesity, infectious disease, anorexia,
 neurodegenerative disorders, Alzheimer's disease and cancer.
 Claim 1; Page 291; 666pp; English.
 The invention relates to human polypeptides, termed NOVX, and the
 polynucleotides encoding them. The polypeptides and polynucleotides are
 useful for diagnosing disease, and screening for potential therapeutic
 agents. The sequences are useful for treating metabolic disorders,
 cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic
 stenosis, atrial septal defect (ASD), atriocentric stenosis, scleroderma,
 ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular
 septal defect (VSD), valve diseases, tuberculous sclerosis, scleroderma,
 atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative
 disorders, Alzheimer's disease, Parkinson's disease, immune disorders,
 haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease
 and cancer. Sequences ABU5452-ABU5467 represent human NOVX polypeptides
 of the invention
 Sequence 399 AA;
 Query Match 61.8%; Score 2102.5; DB 6; Length 399;
 Best Local Similarity 99.0%; Pred. No. 2.3e-163;

Matches 398; Conservative 1; Mismatches 0; Indels 3; Gaps 1;
 QY 1 MDKYDVIKAIQGGAFKAYLAKGKSDSKHCVIKINFEKMPIQKEASKKEVILLERKWKH 60
 DB 1 MDKYDVIKAIQGGAFKAYLAKGKSDSKHCVIKINFEK--QKKEASKKEVILLERKWKH 57
 QY 61 PNIVAFNFSQENGRLFIWVEYCDGDLMKRINRQGVLFSEDOILGFWQISLGLKXHH 120
 DB 58 PNIVAFNFSQENGRLFIWVEYCDGDLMKRINRQGVLFSEDOILGFWQISLGLKXHH 117
 QY 121 DRKILHRDIKAQNIIFLSKNGWAKLGDGFIARVLNNSMELARTICIGTPYYLSPEICQKP 180
 DB 118 DRKILHRDIKAQNIIFLSKNGWAKLGDGFIARVLNNSMELARTICIGTPYYLSPEICQKP 177
 QY 181 YNNKTDIWSLGCVLVELCTIKHPPEGNLQOLVKICQAHFAPISPGFSRELHSLISOLF 240
 DB 178 YNNKTDIWSLGCVLVELCTIKHPPEGNLQOLVKICQAHFAPISPGFSRELHSLISOLF 237
 QY 241 QVSPDRPSINSILKRPFFLENLIPKYLTPVIOEFSHMLICRAGAPASHAGKVKQCK 300
 DB 238 QVSPDRPSINSILKRPFFLENLIPKYLTPVIOEFSHMLICRAGAPASHAGKVKQCK 297
 QY 301 IQKVFQKCPKPSRISVPIKRNAILHRNWRPPAGAKARSIMTERPKIAAVCGHYDY 360
 DB 298 IQKVFQKCPKPSRISVPIKRNAILHRNWRPPAGAKARSIMTERPKIAAVCGHYDY 357
 QY 361 YYAQLDMLRRRAHKPSYHPIQENTGVEDYQETRHGSPSQ 402
 DB 358 YYAQLDMLRRRAHKPSYHPIQENTGVEDYQETRHGSPSQ 399
 RESULT 9
 ADF44515
 ID ADF44515 standard; protein; 614 AA.
 XX AC ADF44515;
 XX DT 12-FEB-2004 (first entry)
 XX DE Mouse kinase protein SEQ ID NO:33.
 XX KW cytotstatic; nootropic; neuroprotective; antidiabetic; screening;
 XX KW regulation; drug development; protein-associated disease; cancer;
 XX KW dementia; diabetes; kinase; enzyme; mouse.
 XX OS Mus musculus.
 XX PN WO2003084992-A1.
 XX PD 16-OCT-2003.
 XX PF 04-APR-2003; 2003WO-JP004330.
 XX PR 05-APR-2002; 2002JP-00103396.
 XX PR 23-APR-2002; 2002JP-00120904.
 XX PR 02-MAY-2002; 2002JP-00130601.
 XX PR 04-DEC-2002; 2002JP-00352520.
 XX PA (RIKE) RIKEN KK.
 XX PA (DNAP-) DNAPFORM KK.
 XX PA (MITU-) MITSUBISHI CHEM CORP.
 XX PI Hayashizaki Y, Kamiya M, Kubodera H, Watanabe W;
 XX WPI; 2003-833568/77.
 XX DR N-PSDB; ADF44489.
 XX PT Proteins and encoded DNAs with kinase activity, useful in screening
 XX PT substances for regulating such activity and in developing drugs for the
 XX PT protein-associated diseases e.g. cancer, dementia and diabetes.
 XX PS Claim 1; SEQ ID NO 33; 342pp; Japanese.
 XX

The present invention describes a protein: (a) containing any of the amino acid sequences of ADF4509 to ADF4534 or ADF4544; or (b) based on any of the sequences in (a) but with some amino acids deleted, substituted and/or added and having kinase activity. Also described: (1) a DNA encoding any of the proteins; (2) a full-length cDNA encoding the protein; (3) a DNA which is: (a) a DNA containing any of the base sequences in ADF4483 to ADF4508 or ADF4543; (b) a DNA derived from any of the sequences in (a) but with some bases deleted, substituted and/or added and encoding a protein with kinase activity; or (c) a DNA hybridizable with any of the sequences in (a) or their complementary strands under stringent conditions and encoding a protein with kinase activity; (4) a recombinant vector containing the DNA; (5) a cell transfected with the DNA or recombinant vector, or an individual produced from the cell; (6) recombinant proteins produced by such cells; (7) an oligonucleotide containing 5-10 consecutive bases in any of the base sequences, its sense oligonucleotide, an antisense oligonucleotide with a complementary strand of such sense oligonucleotide, or an oligonucleotide derivative of the (anti-)sense oligonucleotide; (8) an antibody specifically binding to the protein, or its partial fragment; (9) a method for screening substances for regulating activity of the protein by contacting a test substance with such protein before measuring changes in the protein activity due to the test substance; (10) a method for screening substances regulating expression of the DNA by contacting a test substance with cells transfected with the gene and detecting changes in expression level of the DNA in such cells; (11) recordable media for reading in a computer with information on the amino acid sequences of the proteins, and/or base sequences of the DNAs stored; and (12) a support for binding with any of the proteins and/or DNAs. The proteins and their encoded DNAs have cytostatic, neurotropic, neuroprotective and antidiabetic activities. They can be used in screening substances for regulating such activity and in developing drugs for the protein-associated diseases e.g. cancer, dementia and diabetes. The present sequence is used in the exemplification of the present invention.

Sequence 614 AA;

Query Match 48.2%; Score 1640.5; DB 7; Length 614;
 Best Local Similarity 54.8%; Pred. No. 2.9e-125;
 Matches 340; Conservative 49; Mismatches 72; Indels 159; Gaps 9;

QY 1 MDKTDVKAICQAGFKAYLAKGSDSKHCVKEINFEKMPIOEKESKEVILLKMKH 60
 DB 1 MDNFHLIKIIGEGTFGVYLAOKDSSESHCVKEISLTK----EKEASKNEVILLARMEH 56

QY 61 PNIVAFNFSFOENGRFLFVMEYCDGDLMKRINRQGVLFSEDOILGWVQVLSGLKHH 120
 DB 57 PNIVTFSSFOENGRFLFVMEYCDGDLQRIQQRGVMESEDOILGWVQVLSGLKHH 116

QY 121 DRKILHRDIKAQNTFLSKNGWAKLGDFTGARTVNNMELARTCIGTPYVLSPEICQKP 180
 DB 117 DRKILHRDIKSNITFLSKNGWAKLGDFTGARTVNNMELARTCIGTPYVLSPEICQNP 176

QY 181 YNNKTDIWSLGCVLVECTLKHPPGNNLQOLVLCIQAHFAPISPGFSRELHSLISOLF 240
 DB 177 YNNKTDIWSLGCVLVECTLKHPPGNNLQOLVLCIQAHFAPISPGFSRELHSLISOLF 236

QY 241 QVSPDRPSINSILKRPFLNLIKYLTPTVQIEFSLHMLICRAGAPASRACKVQKCK 300
 DB 237 RVSPQDRPSVTSLLKRPFLNLIKYLTPTVQIEFSLHMLICRAGAPASRACKVQKCK 267

QY 301 IQVFRFRCKPFRSRI SVPIKKNAILHNRNWRPAGAKAARSIKWIERPKIAVCGHYDY 360
 DB 268 -----CSR----- 271

QY 361 YYAQIDMLRRRAHKPSYHPIQENTGVEDYQETRHGESP-----SOWPBYLQKFEAAQ 416
 DB 272 -----IQSHAH-----MENMAI-----GPTACWRVSPWSAAYLQKFEAAQ 307

QY 417 YKLKVEKQLGLRPSAENYVNRQELNSGEPFQELPRKKNEMKQOEYVWQLEIRIQ 476
 DB 308 YKLKVEKQLGLRPSVPEHPNEGKLSHWEETKQELQVRRKNMKDQYKQLEIRIQ 367

QY 477 YLNDMKEIRKKNGREPDIENDLKQMRILQNTKESKNPEQYKAKKGVKFEINLDKCISE 536

DB 368 YHNDMKEIRKKNGRE-----LKRUVKFEISLDKCISE 400
 QY 537 NILOEEAMDIPTNLTTFEDGMKFKYECVKEHGDYTDKAFKHLHCP-----AAF 587
 DB 401 DTVQNEAVDKLNATLSFEDGTKEHCRKEEHEDYTDRAFEELCGPEARGFQDVIAAE 460

QY 588 TELTWLSFLFLEYSLPHLL 607
 DB 461 NRQW-----DAGAPHTLL 474

RESULT 10
 ADF44528
 ID ADF44528 standard; protein; 336 AA.
 XX ADF44528;
 XX 12-FEB-2004 (first entry)
 XX Mouse kinase protein SEQ ID NO:46.
 XX cytotatic; neurotropic; neuroprotective; antidiabetic; screening;
 KW regulation; drug development; protein-associated disease; cancer;
 KW dementia; diabetes; kinase; enzyme; mouse.
 OS Mus musculus.
 XX WO2003084992-A1.
 PN 16-OCT-2003.
 PD 04-APR-2003; 2003WO-JP004330.
 XX 05-APR-2002; 2002JP-00103396.
 PR 23-APR-2002; 2002JP-00120904.
 PR 02-MAY-2002; 2002JP-00130601.
 PR 04-DEC-2002; 2002JP-00352520.
 XX (RIKE) RIKEN KK.
 PA (DNAP-) DNAFORM KK.
 PA (MITU) MITSUBISHI CHEM CORP.
 XX Hayashizaki Y, Kamiya M, Kubodera H, Watanabe W;
 PI WPI; 2003-833568/77.
 XX N-PSDB; ADF44502.
 XX Proteins and encoded DNAs with kinase activity, useful in screening
 PT substances for regulating such activity and in developing drugs for the
 PT protein-associated diseases e.g. cancer, dementia and diabetes.
 XX Claim 1; SEQ ID NO 46; 342pp; Japanese.
 CC The present invention describes a protein: (a) containing any of the
 CC amino acid sequences of ADF4509 to ADF4534 or ADF4544; or (b) based on
 CC any of the sequences in (a) but with some amino acids deleted,
 CC substituted and/or added and having kinase activity. Also described: (1)
 CC a DNA encoding any of the proteins; (2) a full-length cDNA encoding the
 CC protein; (3) a DNA which is: (a) a DNA containing any of the base
 CC sequences in ADF4483 to ADF4508 or ADF4543; (b) a DNA derived from any
 CC of the sequences in (a) but with some bases deleted, substituted and/or
 CC added and encoding a protein with kinase activity; or (c) a DNA
 CC hybridizable with any of the sequences in (a) or their complementary
 CC strands under stringent conditions and encoding a protein with kinase
 CC activity; (4) a recombinant vector containing the DNA; (5) a cell
 CC transfected with the DNA or recombinant vector, or an individual produced
 CC from the cell; (6) recombinant proteins produced by such cells; (7) an
 CC oligonucleotide containing 5-10 consecutive bases in any of the base
 CC sequences, its sense oligonucleotide, an antisense oligonucleotide with a
 CC complementary strand of such sense oligonucleotide, or an oligonucleotide
 CC derivative of the (anti-)sense oligonucleotide; (8) an antibody
 CC specifically binding to the protein, or its partial fragment; (9) a

CC method for screening substances for regulating activity of the protein by
 CC contacting a test substance with such protein before measuring changes in
 CC the protein activity due to the test substance; (10) a method for
 CC screening substances regulating expression of the DNA by contacting a
 CC test substance with cells transfected with the gene and detecting changes
 CC in expression level of the DNA in such cells; (11) recordable media for
 CC reading in a computer with information on the amino acid sequences of the
 CC proteins, and/or base sequences of the DNAs stored; and (12) a support
 CC for binding with any of the proteins and/or DNAs. The proteins and their
 CC encoded DNAs have cytostatic, neurotropic, neuroprotective and antidiabetic
 CC activities. They can be used in screening substances for regulating such
 CC activity and in developing drugs for the protein-associated diseases e.g.
 CC cancer, dementia and diabetes. The present sequence is used in the
 CC exemplification of the present invention.

XX
 SQ Sequence 336 AA;

Query Match 33.4%; Score 1135.5; DB 7; Length 336;
 Best Local Similarity 77.0%; Pred. No. 2.9e-84;
 Matches 217; Conservative 22; Mismatches 36; Indels 7; Gaps 2;

QY 1 MKYDVVKAIGCAFAGKAYLAGKSDSKHCVIKEINFEKMPIQEKESKKEVILLKMKH 60
 DB 1 MDNFHLIKIIGTGTGKVLAKDKSESSHCVKEISLTK----EKESKNEVILLARMEH 56
 QY 61 PNIVAFENFQNGRLFIWVEYCDGDLMKRINRQGVLFSDQILGWFVQISLGLKH 120
 DB 57 PNIVTFSSQNGRLFIWVEYCDGDLMKRINRQGVLFSDQILGWFVQISLGLKH 116
 QY 121 DRKILHRDIKAQNIFLSKNGMVAKLGDGFIARVLNNSMELARTCTGTPYLSPEICQNK 180
 DB 117 DRKILHRDIKQNIFLSKNGMVAKLGDGFIARTLNSMELAQTCAGTPYLSPEICQNR 176
 QY 181 YNNKTTDINSGLCVLYELCTLKHPPFEGNNLQQLVLKICQAHFAPISPGFSREHLISL 240
 DB 177 YNNKTTDINSGLCVLYELCTLKHPPFESNNFHLVLKICQGRVAPISPHFSRDLSLP 236
 QY 241 QVSPDRPRPSINSILKRPFLNIPKYLTPVQI---EBFSM 279
 DB 237 RVSPQDRPSVTLKRPFLNIPKYLTPVQI---EBFSM 278

RESULT 11

ABP96073
 ID ABP96073 standard; protein; 544 AA.
 AC ABP96073;
 XX
 DT 07-MAY-2003 (first entry)
 DE Human protein kinase SEQ ID NO:52.
 XX

Human; protein kinase; enzyme; antiaesthatic; antiinflammatory;
 KW antidiabetic; antiparkinsonian; antimigraine; cardiant; cytostatic;
 KW immunosuppressive; vulnary; gene therapy; COPD; asthma; migraine;
 KW chronic obstructive pulmonary disease; non-insulin dependent diabetes;
 KW Parkinson's disease; myocardial infarction; inflammatory bowel disease;
 KW autoimmune disorder; allograft rejection; graft versus host disease;
 KW cancer; leukaemia; wound granulation.

OS Homo sapiens.

XX WO2003000901-A2.

PN 03-JAN-2003.

XX 24-JUN-2002; 2002WO-IB002358.

PF 26-JUN-2001; 2001US-0301098P.

PR 06-NOV-2001; 2001US-0332870P.

XX (DECO-) DECODE GENETICS EHF.

XX

PI Martinez RAM, Sigurdson GT;

XX WPI; 2003-201429/19.

DR N-PSDB; ABZ77151.

XX New protein kinase genes and polypeptides, useful for diagnosing diseases
 PT associated with a protein kinase, or in gene therapy for treating e.g.
 PT Parkinson's disease, migraine, myocardial infarction, allograft rejection
 PT or cancers.

PS Claim 9; Page 75-76; 258pp; English.

XX ABZ77126 to ABZ77185 encode the human protein kinases given in ABP96048
 CC to ABP96087. The protein kinases have antiaesthatic, antiinflammatory,
 CC antidiabetic, antiparkinsonian, antimigraine, cardiant, cytostatic,
 CC immunosuppressive and vulnary activities, and can be used in gene
 CC therapy. A protein kinase therapeutic agent from the present invention,
 CC particularly a protein kinase gene agonist or antagonist, can be used for
 CC treating a disease or condition associated with a protein kinase in an
 CC individual. These diseases include chronic obstructive pulmonary diseases
 CC (COPD), asthma, non-insulin dependent diabetes, Parkinson's disease,
 CC migraine, myocardial infarction, inflammatory bowel disease, autoimmune
 CC disorders (e.g. allograft rejection or graft vs. host disease), cancers
 CC (e.g. leukaemias) or wound granulation

XX Sequence 544 AA;

Query Match 32.6%; Score 1108.5; DB 6; Length 544;
 Best Local Similarity 55.6%; Pred. No. 9.2e-82;
 Matches 237; Conservative 8; Mismatches 22; Indels 159; Gaps 5;

QY 10 IQGAP--GKAYLAGKSDSKHCVIKEINFEKMPIQEKESKKEVILLKMKHPIVAF 67
 DB 16 VGLGVFLRGVAYRAKRGDGEWLL-----SGAVKHMALIKMAD-----KYL 58
 QY 68 NSFO-----ENGLFIWVEYCDGDLMKRINRQGVLFSDQILGWFVQISLGLKHI 119
 DB 59 KSFQHQMIPLTENGRLFIWVEYCDGDLMKRINRQGVLFSDQILGWFVQISLGLKHI 118
 QY 120 HDRKILHRDIKAQNIFLSKNGMVAKLGDGFIARVLNNSMELARTCTGTPYLSPEICQNK 179
 DB 119 HDRKILHRDIKAQNIFLSKNGMVAKLGDGFIARVLNNSMELARTCTGTPYLSPEICQNK 178
 QY 180 PYNKTTDINSGLCVLYELCTLKHPPFEGNNLQQLVLKICQAHFAPISPGFSREHLISL 239
 DB 179 PYNKTTDINSGLCVLYELCTLKHPPFEGNNLQQLVLKICQAHFAPISPGFSREHLISL 238
 QY 240 FQVSPDRPRPSINSILKRPFLNIPKYLTPVQIEBFSHMLICRAGAPASRHAGKVQXC 299
 DB 239 FQVSPDRPRPSINSILKRPFLNIPKYLTPV----- 270
 QY 300 KIQVFRGKCPSPRSRISVPIKENALHREWPPAGAQKARSIKMERPKIAVCGHYD 359
 DB 271 ----- 270
 QY 360 YYVAQLDMLRRRAHKPSYHPIPOENTGVEDYDQETRHGSPSPQWPAEYLRKFEAQYKL 419
 DB 271 -----SPEYLQRKFEAQYKL 286
 QY 420 KVEKQL 425
 DB 287 KVEKQL 292

RESULT 12

AAM39210
 ID AAM39210 standard; protein; 1242 AA.
 XX AAM39210;
 AC AAM39210;
 XX
 DT 22-OCT-2001 (first entry)
 XX Human polypeptide SEQ ID NO 2355.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.

OS Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-00488725.

XX 25-APR-2000; 2000US-0052317.

XX 20-JUN-2000; 2000US-00598042.

XX 19-JUL-2000; 2000US-00620312.

XX 03-AUG-2000; 2000US-00653450.

XX 14-SEP-2000; 2000US-00662191.

XX 19-OCT-2000; 2000US-00693036.

XX 29-NOV-2000; 2000US-00727344.

(HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D; Zhang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA; Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

XX N-PSDB; AAI58366.

XX Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.

XX Example 4; SEQ ID NO 2355; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification

XX Sequence 1242 AA;

Query March 31.9%; Score 1086; DB 4; Length 1242;

Best Local Similarity 32.7%; Pred. No. 2e-79;

Matches 278; Conservative 122; Mismatches 197; Indels 254; Gaps 21;

Qy 1 MDKDVTKAIGQAGFAYLAKSDSKVCHVKEINFEKMPFIOKEAKKEVILLKMKH 60

Db 1 MEKTVRLQKIGESFGKAILVKSTEDGQYVKEINISVSKERESREVAVLANMKH 60

Qy 61 PNIVAFNPSFQENGLRITVMEYDCGGLMKRINRQGVLSFSDQILGNFVQISLGLKH 120

Db 61 PNIVQYRESPFENGSLIVMDYDCGGLFKRINAQGVLFQEDQILDMFVQICLALKGHV 120

Qy 121 DRKILHRDIKAQNIPLSKNGMVAKLDFGFIARVLNNSMELARTICIGTPYLSPEICNKP 180

Db 121 DRKILHRDIKSNIFLFDKGTV-QLGDFGIARVLNLSVELARTICIGTPYLSPEICENKP 179

Qy 181 YNNKTDIWSLGCVLVELCTLKHPPFEGNNLQOLVKIQAHFAPISPGFSRELHSLLSQLF 240

Db 180 YNNKSDIWAISLGCVLVELCTLKHAFAGSMKNLVLKIISSGSPVPSLHYSYDLASLSQLF 239

Qy 241 QVSPRDRPSINSILKRPFLNLPKYLTPVQIEPSPHMLICRAGA---PASHAG--- 293

Db 240 KRNPRDRPSVNSILEKGFIAKRIEKLFLSPOLIAEEFLKTFSPGQPIFAKPASQNS 299

Qy 294 -KVQKCKIQVFRFGKCPSPRSISVPI-----KRNAILHRNWRPP----- 334

Db 300 ISVMPAQKITK-----PAKYGIPLAYKYGDKKLHEKPLQKHQAHTPEKRVNT 351

Qy 335 -----AGAKARSIMIER----- 348

Db 352 GEERRKISEEAARKRLFEIEKEKKQDKQIISLMKAEQMKRQEKERLERINRAEQQWRN 411

Qy 349 -----PXIAAVCGHYDYVYAQLDMLRRRAHKPSVHPPIQENTG 386

Db 412 VLSAGSGEVKAPFLGGGTTAPSSFSRGOYEHYHAIQMQOQRAEDN-----EAKWK 466

Qy 387 VEDYG-----QETRHGSPSPQPAEYQKFEAQYKLVKVEKQLGL-----RPS 430

Db 467 REIYGRGLPERQKGLAVERAKQVEEFLQKREAMQNKARAEHGMILQNLAAAMYGRPS 526

Qy 431 SAEPNYNQRELRSNGBEPRFQELPFKRNEMKEQYWKOLEEIRQOYLNDMKEIRKQWR 490

Db 527 S-----SRGKPRNKE-----EEVYLARLQIRLQNFNERQIQAKLRG 565

Qy 491 EPEDI-----EKDKQMLQNTK-----ESKNPE-----QKY 517

Db 566 EKKEANHSEGOEGSEADMRKKTIESLKAHANARAAVLKEQLERKKEAYEREKVVWEH 625

Qy 518 KAKGVKF-----EINLDKISDENILQEE--- 542

Db 626 LVAKGVKSDVSPPLQGHETGSPSKQOMRSVITSALKEVGVDSLTDTRETSEMQK 685

Qy 543 -----EAMDIPNETLTPEDGMKFE-----YECVKEHGDYTDKAPEKLHCP 583

Db 686 TNNAISSKKEILRLNENLKAQDEKQKQNLSDTFEINVHEDAKEHEKESVSDRKKW- 744

Qy 584 EAAFTLWLSFLFLEYSLPFLLEKSPFSSHLLIEDLL-----CANDCSLK 629

Db 745 EAGGQVLPDLDELATLDTSF-----STTERHTVGEVILKLPNGSPRRAMGKSPTDSVLX 797

Qy 630 DWSEKEMELRT 640

Db 798 ILGEAELQLOT 808

RESULT 13

AAO16440

ID AAO16440 standard; protein; 1242 AA.

XX AAO16440;

XX 10-APR-2003 (first entry)

XX Human serine/threonine protein kinase NEK1.

XX Human; gene therapy; serine/threonine protein kinase; NEK1; cancer; colon cancer; cardiovascular disorder; congestive heart failure; disease; central nervous system disorder; chronic obstructive pulmonary disease; CNS disorder; diabetes; myocardial infarction; ischaemic heart disease; arrhythmia; hypertensive; Alzheimer's disease; Parkinson's disease; peripheral pain; chronic pain.

XX Homo sapiens.

XX WO2003000873-A2.

XX 03-JAN-2003.

PF	21-JUN-2002; 2002WO-BP006879.	
XX	25-JUN-2001; 2001US-0300071P.	
PR	16-NOV-2001; 2001US-0331447P.	
PR	07-DEC-2001; 2001US-0336693P.	
XX	(FARB) BAYER AG.	
PA		
XX		
XX	Xiao Y;	
PI		
XX	WPI; 2003-201424/19.	
DR	N-P8DB; AAL51590.	
XX		
PT	New serine/threonine protein kinase NEK1 gene and protein, useful for	
PT	identifying modulators of serine/threonine protein kinase NEK1 activity,	
PT	and in gene therapy for treating cancer, diabetes, heart failure or	
PT	Alzheimer's disease.	
XX		
PS	Claim 1; Fig 2; 156pp; English.	
XX		
CC	The invention comprises the amino acid and coding sequence of the human	
CC	serine/threonine protein kinase NEK1. The DNA and protein sequences of	
CC	the invention are useful for modulating the activity of serine/threonine	
CC	kinase NEK1 in a disease, such as: cancer (particularly colon cancer);	
CC	cardiovascular disorders; central nervous system (CNS) disorders;	
CC	diabetes; and chronic obstructive pulmonary disease. In particular the	
CC	DNA and protein sequences of the invention are useful for treating:	
CC	congestive heart failure; myocardial infarction; ischaemic heart disease;	
CC	arrhythmia; hypertensive; Alzheimer's disease; Parkinson's disease; and	
CC	peripheral or chronic pain. The present amino acid sequence represents	
CC	the human serine/threonine protein kinase NEK1 of the invention	
XX		
SQ	Sequence 1242 AA;	
Query Match		
Best Local Similarity 31.9%; Score 1086; DB 6; Length 1242;		
Matches 278; Conservative 122; Mismatches 197; Indels 254; Gaps 21;		
QY	1 MDKYVIRKAIAGGAFKAYLAKGSDSKHCIVIKIEINFEKMPDQKEASKVEVILLKMKH 60	
Db	1 MEKYVRLQIKGSGFKAILVKSTEDGRQYVKEINISMSKKEESRREVAVLANMKH 60	
QY	61 PHIVAFNSFQNGRLFIWMEVCDGDLWKINRQGVLFSDQILGWVQISLGLKHII 120	
Db	61 PHIVQRESFEENGLYIMVDYCEGDLFKRINAQGVLFQBDQILDWFVQICLAKHVV 120	
QY	121 DRKILHRDIKAQNIFLSKNGMVAKLGDGFIARLVNLSMELARTCIGTPYILSPICQNKP 180	
Db	121 DRKILHRDIKSNIFLTKDGTV-QLGDGFIARLVNSTVLEARTCIGTPYILSPICENKP 179	
QY	181 YNNKTDIWSLGCYVLELCTLKHPPFGNNLQQLVKICOAHFAPISPGFSRELHSLISOLF 240	
Db	180 YNNKSDIWAIGCVLYELCTLKHAFAGSMKNVLKIIISGSPFPVSLHYSYDLRSIVLSOLF 239	
QY	241 QVSPDRDSINILKRPFLNLIKVLTPVETIQEFSHMLICRAGA---PASRHAG--- 293	
Db	240 KNPDRDRSVNSILEKGIKRIEFLSPQLIAEEFCLKTFSGSQIPAKRPFASQNS 299	
QY	294 -KVVQKCKIQVRFKGPSPRSISVPI-----KRNAILHENEWRPP----- 334	
Db	300 ISVMPAQKITK-----PAKYGIPLAYKYGDKLHKPLQKHQAQHTPEKRYNT 351	
QY	335 -----AGAQKARSIMIER----- 348	
Db	352 GEERKISBEAARKRLRLEIEKEKQKQDIIISLMAEQMKRQKERLERINRAREQWRN 411	
QY	349 -----PKIAAVCGHYDYVYQALDMLRRRAHKPSVHPPIQENTG 386	
Db	412 VLSAGSGEVKAPFLGSGGTAPISFSRSGQYEHVHAIFDQMQQRAEDN-----EAKWK 466	
QY	387 VEDYG-----QETHRGSPSQWPAEYLQRPFAQYKLVKEQKGL-----RPS 430	
Db	467 REIYGRGLPERQKGLAVERAKQVEEFLQKRREANQKARAEHGMILQNLAAAMYGGRRPS 526	

QY	431	SABPNYNQROELRSNGEPRFQELPRKKNMKQOEYKWKQLEIRQQVYLNMDKMKIRKQMR	490
Db	527	S-----SRGKPRNKE-----EEVYLARLQIRLQNFNERQQIKAKLRG	565
QY	491	EPEDI-----EKDLAQMBLQNTK-----ESKNPE-----OKY	517
Db	566	EKEANHSQEGSESEADMRKKIESLKAHANARAVALKEQLERKKEAYERKKVWEEH	625
QY	518	KAKGVKF-----EINLDKICISDENILOEE--- 542	
Db	626	LVAKGVKSDVSPPLGQHETGSGSPKQMSRVSIVTSALKVEGVDSLTDTRETSEMQK	685
QY	543	-----BAMDIPNETLTTFEGMKFKE-----YECVKEHGDYTDKAFKHLCP	583
Db	686	TNNAISKRIILRLNENLKAQDEKQKQNLSTFTFINVHEDAKEHEKESVSSDRKKW-	744
QY	584	EAAPTTLTWLSFLFLEYSLEHFLLEKSPFSRHILIEDLL-----CANDCSLK	629
Db	745	EAGQQLVPLDELTLDTSF-----STTERTVGEVILKLPNGSPRAWGKSPDTSVLK	797
QY	630	DWSEKEMELRT 640	
Db	798	ILGEAELOQT 808	
RESULT 14			
ID	AA026613	standard; protein; 774 AA.	
XX	AA026613;		
XX	28-MAR-2003 (first entry)		
DE	Serine/threonine protein kinase-like enzyme related mouse protein.		
KW	Cytostatic; antiparkinsonian; neurotropic; neuroprotective; cardiatic;		
KW	hypotensive; antiarrhythmic; antianginal; analgesic; antiinflammatory;		
KW	antidiabetic; tranquiliser; antitumor; antidepressant; uropathic;		
KW	anorectic; serine/threonine protein kinase; enzyme; cancer;		
KW	central nervous system disorder; cardiovascular disorder; diabetes;		
KW	chronic obstructive pulmonary disease; obesity; genito-urinary system;		
XX	pain; genetic testing; mouse.		
OS	Mus musculus.		
XX	WO200299096-A1.		
PD	12-DEC-2002.		
XX	06-JUN-2002; 2002WO-BP006203.		
PR	07-JUN-2001; 2001US-0296164P.		
PR	19-SEP-2001; 2001US-0323100P.		
PR	25-OCT-2001; 2001US-0330578P.		
PR	17-JAN-2002; 2002US-0348601P.		
XX	(FARB) BAYER AG.		
XX	Smolyar A, Horner EJ, Thelwell C;		
XX	WPI; 2003-140620/13.		
XX	New human serine/threonine protein kinase-like enzyme polypeptide and		
PT	polynucleotide, useful for regulating the activity of the protein kinase-		
PT	like enzyme to prevent, treat or ameliorate diabetes, cancer or obesity.		
XX	Disclosure; Fig 3; 157pp; English.		
XX	The invention relates to an isolated polynucleotide comprising: a		
CC	polynucleotide encoding a serine/threonine protein kinase-like enzyme		
CC	polypeptide; a sequence of 840, 990, 1120, 2142, or 1383 base pairs fully		
CC	defined in the specification; a polynucleotide that hybridises to the		

CC serine/threonine protein kinase-like enzyme DNA or a fragment thereof; or
CC a degenerate analogue of the said polynucleotides. The serine/threonine
CC protein kinase-like enzyme polypeptide and polynucleotide are useful in
CC preventing, ameliorating, or treating diseases associated with serine/
CC threonine protein kinase-like enzyme dysfunction such as cancer, central
CC nervous system disorders, cardiovascular disorders, chronic obstructive
CC pulmonary disease, diabetes, obesity, or disorders of the genito-urinary
CC system. These can also be used to treat pain associated with the above
CC disorders. The serine/threonine protein kinase-like enzyme polypeptide is
CC also useful in diagnostic assays or in genetic testing. The expression
CC vector or the reagent is useful in preparing a medicament for modulating
CC the activity of a serine/threonine protein kinase-like enzyme in a
CC disease, e.g. cardiovascular disorder, obesity, a disorder of the genito-
CC urinary system, a central nervous system disorder, diabetes, cancer, or
CC chronic obstructive pulmonary disease. The methods are useful in
CC producing and detecting the polynucleotide and polypeptide and in
CC screening for agents that modulate the activity of the serine/threonine
CC protein kinase-like enzyme polypeptide. This sequence represents a mouse
CC protein relating to the serine/threonine protein kinase-like enzyme
CC of the invention
XX
XX
SQ . Sequence 774 AA;

Query Match 31.7%; Score 1078; DB 6; Length 774;
Best Local Similarity 36.4%; Pred. No. 4.7e-79;
Matches 260; Conservative 107; Mismatches 171; Indels 176; Gaps 21;

QY 1 MDKVDVKAIGOGAFGKAYLAKGSDSKHCVKEINFEKMPIOEKASKKEVILLKMKH 60
DB 1 MEKVRLQKIGEGFGKAVLVKSTEDGRHYVKEINISMSDKERQESREAVLANMKH 60

QY 61 PNIVAFNSFOENGRLEFIVMEYCDGDLMKRINRQGVLFSEDIQILGWFWQISGLKHH 120
DB 61 PNIVQYKESFEENGLYIMVDCGGDLFKRINAQKALFQEDQILDWFVQICLAKHVV 120

QY 121 DRKILHRDIKAQNTFLKNGWAKLGFGIARVLNNSMELARTICIGTPYLSPEICQNP 180
DB 121 DRKILHRDIKSONLFTKGTV-QLGFQGIARVLNSTVELARTICIGTPYLSPEICENP 179

QY 181 YNNKTDIWSLCVLYELCTLKHPEGNLQOLVLKICQAHFAPISFGSRELSLSQLF 240
DB 180 YNNKSDIHALGCVLYELCTLKHAFEGAGNKNLVKTISSGFPVPSHYSDLSLSQLF 239

QY 241 QVSPDRPSINSILKRPFLNLPKYLTPVTEIQRSHMLICRAG----- 285
DB 240 KRNPRDRPSVNSILKRFIAKIEKFLUSPOLIAEEFCLKTLSPFGQPLPGKRPASGGV 299

QY 286 -----APASRHAGVVKCKIQKVRFGKCPSPRSIS--VPIKRNAILHRNEWRP 333
DB 300 SSFVPAQKITPAKYGVPLTYKYGDKLLEKPPKPKQAQHPVK--MNSGEERK 356

QY 334 PAG--AKAKSIKMIER----- 348
DB 357 KMSEAAKGRLEFIEKEKQKQDQIRFLKAEQMKRQEKQLERINRAREGWNVLRAAG 416

QY 349 -----PKIAVCHYDYVAQLDMLRR-RAH-----KPSYHP--IPQ 383
DB 417 SGEVYKASFFGIGGAVSPSPCGQYEHYHAI PQMQRLEAEDNEARWKGGIYRWLPER 476

QY 384 NTG---VEDYQETRHGSPSQWPAEYLQKRFQAYKLVK-----KOLGURPS 431
DB 477 QKQHLAVERANQ-----VEEFQKREAMQNKARAEHVVYLAFLRLQIRLQ--- 522

QY 432 AEPYNVQRQELR-----SNGEPRFQBLPRKNMEKEQEWKQLEBIRQOYLN 479
DB 523 ---NFNERQQIKALRGKENKADTKQCBAT-BETDVR-----LKWSGLKQATNARAVLK 575

QY 480 DMKEIRKMGREPEDIEKDLQKQELQNTKESKNP-----BQYKAKKGVKF--- 525
DB 576 EQLERKEKAYERE--KKWEEHLVARVKSQVPLPLELLETGSPSPSKQVQKPVISGTA 633

QY 526 --EINLKKCSDENILQEEAMQIPNETLT-----PEDGMKFYEYECVKEH 569

Db 634 LKEVLDGLSDT----TQEEEMKSNAGSISKREILRLNENLKAQDEKEKQH 683

RESULT 15
ABP71711
ID ABP71711 standard; protein; 774 AA.
AC ABP71711;
XX
DT 17-APR-2003 (first entry)
XX
DE NEK-like serine/threonine protein kinase NEK1_mouse # SEQ ID 3.
XX
NEK-like serine/threonine protein kinase; cytostatic; cardiant;
KW antiinflammatory; nontropic; neuroprotective; cancer; colon cancer;
KW cardiovascular disorder; diabetes; COPD; CNS disorder; mouse; rat.
XX
OS Mus musculus.
OS Rattus norvegicus.
XX
PN WO2003000903-A2.
XX
PD 03-JAN-2003.
XX
PF 24-JUN-2002; 2002WO-EP006948.
XX
PR 25-JUN-2001; 2001US-0300068P.
PR 07-DEC-2001; 2001US-0336704P.
XX
PA (FARB) BAYER AG.
XX
PI Xiao Y;
XX
DR WPI; 2003-184051/18.
XX
PT New polynucleotide encoding a NEK-like serine/threonine kinase
PT polypeptide useful for treating diseases associated with kinase
PT dysfunction, e.g. cardiovascular disorders, cancer such as colon cancer,
PT diabetes and CNS disorders.
XX
PS Disclosure; Fig 3; 149pp; English.
XX
CC The invention relates to a newly isolated polynucleotide encoding an NEK-
CC like serine/threonine protein kinase. The activity of the polynucleotide
CC and polypeptide of the invention may be described as cytostatic,
CC cardiant, antiinflammatory, nontropic and neuroprotective. The expression
CC vector and reagent of the invention are useful for the preparation of a
CC medicament for modulating the activity of an NEK-like serine/threonine
CC kinase in a disease, such as cancer (e.g. colon cancer), cardiovascular
CC disorder, diabetes, COPD or CNS disorder. The polypeptides may also be
CC used to identify compounds which may act as activators or inhibitors at
CC the enzyme's active site, to raise specific antibodies which can block
CC the enzyme and effectively reduce its activity, as a bait protein in a
CC two-hybrid or three-hybrid assay to identify other proteins which bind to
CC and interact with the human NEK-like serine/threonine kinase polypeptide
CC and modulate its activity, and for the immunisation of mammals. The
CC current sequence represents an NEK-like serine/threonine protein kinase
CC designated NEK1_mouse
XX
SQ . Sequence 774 AA;

Query Match 31.7%; Score 1078; DB 6; Length 774;
Best Local Similarity 36.4%; Pred. No. 4.7e-79;
Matches 260; Conservative 107; Mismatches 171; Indels 176; Gaps 21;

QY 1 MDKVDVKAIGOGAFGKAYLAKGSDSKHCVKEINFEKMPIOEKASKKEVILLKMKH 60
DB 1 MEKVRLQKIGEGFGKAVLVKSTEDGRHYVKEINISMSDKERQESREAVLANMKH 60

QY 61 PNIVAFNSFOENGRLEFIVMEYCDGDLMKRINRQGVLFSEDIQILGWFWQISGLKHH 120
DB 61 PNIVQYKESFEENGLYIMVDCGGDLFKRINAQKALFQEDQILDWFVQICLAKHVV 120

Search completed: November 12, 2004, 13:03:04
Job time : 162 secs

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2004, 20:25:58 ; Search time 9743 Seconds
(without alignments)
11503.293 Million cell updates/sec

Title: US-10-730-010-1
Perfect score: 2370
Sequence: 1 ctgtggagaccatggataag.....ctgtcatgccgttacgagcg 2370

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hhg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2370	100.0	2370	6	AR269117
2	2370	100.0	2370	6	AR487609
3	1665	70.3	2240	6	AX394707
4	1656.2	69.9	1965	6	AX394705
5	1654	69.8	2052	6	AX394703
6	1619	68.3	2249	9	BC063885
7	1449.4	61.2	1947	6	AX166554
8	1349	56.9	1918	6	AX659639
9	1338	56.5	1896	6	AX659636
10	696.2	29.4	3835	6	CQ843384
11	696.2	29.4	3835	9	AK126330
12	602	25.4	1632	6	AX803389
13	597.4	25.2	2281	10	BC053516
14	576.2	24.3	1884	6	CQ732078
15	369.4	15.6	1745	9	BC068201
16	369.4	15.6	5426	6	AX224518
17	369.4	15.6	5448	6	AR338755
18	369.4	15.6	5497	9	AB067488
19	369.4	15.6	5508	6	AX658014

20	369.4	15.6	5511	9	HSM800531
21	369.4	15.6	5532	6	AR338754
22	368	15.5	3645	6	AX224471
23	368	15.5	3729	6	AX658011
24	355.8	15.0	4263	6	AR223879
25	355.8	15.0	4263	10	S45828
26	355.8	15.0	5479	10	AK173292
27	288.6	12.2	958	5	CR386196
28	272.8	11.5	187691	9	AL139082
29	255.2	10.8	2369	5	BC075119
30	234.6	10.7	1578	6	AX657957
31	254.2	10.7	1581	6	AX657962
32	254.2	10.7	2110	6	AX504240
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ALIGNMENTS

RESULT 1
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LOCUS AR269117 2370 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1 from patent US 6500656.
ACCESSION AR269117
VERSION AR269117.1 GI:29699967
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2370)
Webster M., Yan, C., Di Francesco, V. and Beasley, E.
AUTHORS Isolated human kinase proteins, nucleic acid molecules encoding
TITLE human kinase proteins, and uses thereof
JOURNAL Patent: US 6500656-A 1 31-DEC-2002;
FEATURES Location/Qualifiers
source 1..2370
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	CATTGGAGACCATGATAGTACGATGATTAAGGCCATCGGGCAAGGTGCCTTCGGGA	60
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Qy	181	AGATGAAACATCCCAACATTTAGCTTCTTCAATTCATTTCAAGAGATGGCAGGCTGT	240
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[illegible]

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Db	1381	GG	AAAAACGAAATGAAGGAACAGGAATATTGGAAAGCAGTTTAGAGGAAATACGCCAACAGT	1440
Qy	1441	AC	CTCAATGACATGAAGAAGAAATTTAGAAAGAGATGGGAGAGAACACAGAGGACATTGAAA	1500
Db	1441	AC	CTCAATGACATGAAGAAGAAATTTAGAAAGAGATGGGAGAGAACACAGAGGACATTGAAA	1500
Qy	1501	AA	GACTTTGAAACAAATGAGGCTTCAGAAACACAAAGGAAGCTTAAAAATCCAGAAACAGAAAT	1560
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Qy	1621	AC	ATCTCCAAAGAGGAGGCAATGATATACCAATGAAACTTTGACCTTTGAGGATG	1680
Db	1621	AC	ATCTCCAAAGAGGAGGCAATGATATACCAATGAAACTTTGACCTTTGAGGATG	1680
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Qy	1861	TT	GAGATCTCCTTTGTGCCAACGACTGCTCACTGAAGCACTGGAGTGAAGGAAATGG	1920
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Qy	2041	GA	AGGCCAGATCAGGGTTTTCCACGCAGACTGTAGTTCTGTGGGAAACAGGAGCGAGT	2100
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Db	2101	GG	ATGGAGAGCGCTCAGACTCTCTCGAGATGTCGATGGCGGACATCACTTCCA	2160
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Db	2161	CT	GTGCCACCGGGCTGACAGTGAGTCTGTGCTTAGTGTACGTCTGAGGAGGGAAGA	2220
Qy	2221	CCA	AGGACCGGTACAGCCAGTCTCATCTCGATGTGATGCTACTTCTCATATACAC	2280
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Db	2281	CC	TATAGATCTTGATCAGACCTTTCAAATATGTTGTTTGTGATATCTCAAGAAAAAAA	2340
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DEFINITION	Sequence 1 from patent US 6706510.				
ACCESSION	AR487609				
VERSION	AR487609.1	GI:47252885			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	Webster,M., Yan,C., Di Francesco,V. and Beasley,E.				
TITLE	Isolated human kinase proteins				
JOURNAL	Patent: US 6706510-A 1 16-MAR-2004;				
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Qy	61	AAGCATCTTAGCTAAAGGGAATCAGATAGCAAGCACTGTGTCATAAAGAGATCAATT	120		
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Qy	121	TTGAAAAGATGCCCATACAGAAAAGAGCTTCAAGAAAAGAGTGTATCTTCGGAAA	180		
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Db	241	TTATTTGTAATGGAATTTGTGATGAGGGGATCTCATGAAAAGGATCAATAGACAAAGGG	300		
Qy	301	GTGTGTTATTAGTGAAGATCAGATCTCGGTGGTGTGATGAGATTTCTTAGAGCTAA	360		
Db	301	GTGTGTTATTAGTGAAGATCAGATCTCGGTGGTGTGATGAGATTTCTTAGAGCTAA	360		
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Db	361	AACATATTTCATGACAGGAAGATATTACACAGGACATATAAGGCTCAGAACATTTTCTTA	420		
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Qy	481	CCATGGAACCTTGCTCGAATCTGTATTGGAACACCTTACTACTCTGCCAGAGATCTGTC	540		
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Db	781	CTTTTGTAGAGATCTTATTTCCCAATATTTTGACTCTGAGGTCAITTCAGGAAGATTCA	840
Qy	841	GTACATGCTTTATATGCAGAGCAGGAGCGCAGCTTCTCGACATGCTGGGAAGGTGCTCC	900
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Db	901	AGAAGTGTAAATAACAAAAGTGCAGATTCCGGGAAAGTCCCAACCAAGATCAAGGATAT	960
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Qy	1441	ACCTCAATGACATGAAAGAAATTTAGAAAGAGATGGGGAGAGAACCCAGAGGACATTGAAA	1500
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Db 1921 AGCTTAGGACATAACCCCTACCACTACATAAACAACCTTTTGAGAAATCAGGAGAGATAA 1980
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RESULT 3
AX394707 2240 bp DNA linear PAT 18-MAY-2002
LOCUS Sequence 5 from Patent WO0218555.
ACCESSION AX394707
VERSION AX394707.1 GI:21065808
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Friddle, C.J., Hilbun, E., Nepomnichy, B. and Hu, Y.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: WO 021855-A 5 07-MAR-2002;
Lexicon Genetics Incorporated (US)
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QY 481 CCATGGAACTTTGCTCGAACTTGTATTGGAAACACCTTACTACTCTGCTTGGCTGTCTTATATGAGC 540
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DEFINITION			
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ACCESSION			
AX394705			
VERSION			
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KEYWORDS			
Homo sapiens (human)			
SOURCE			
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ORGANISM			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
1			
Friedle C.J., Hilbun E., Nepomnichy B. and Hu Y.			
AUTHORS			
Human kinase proteins and polynucleotides encoding the same			
TITLE			
Patent: WO 0218555-A 3 07-MAR-2002;			
JOURNAL			
Lexicon Genetics Incorporated (US)			
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Location/Qualifiers			
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Best Local Similarity 96.1%; Pred. No. 0;			
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RESULT 5
AX394703
LOCUS AX394703
DEFINITION Sequence 1 from Patent WO0218555.
ACCESSION AX394703
VERSION AX394703.1 GI:21065806
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Friddle, C.J., Hilbun, E., Nepomnichy, B. and Hu, Y.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: WO 021855-A 1 07-MAR-2002;
Lexicon Genetics Incorporated (US)
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Location/Qualifiers
Source 1..2052
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ORIGIN
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Matches 1763; Conservative 0; Mismatches 10; Indels 93; Gaps 1;

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QY 72 GCTAAAGGAAATCAGATAGCAAGACATGTGTCTATAAAGAGATCAATTTTGAAGATG 131
Db 61 GCTAAAGGAAATCAGATAGCAAGACATGTGTCTATAAAGAGATCAATTTTGAAGATG 120
QY 132 CCATACAAAGAAAAGAGCTTCAAGAAAAGAGTATCTTCTGGAAAAGATCAAAACAT 191
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RESULT 6
LOCUS BC063885
DEFINITION Homo sapiens similar to Serine/threonine-protein kinase Nek1
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ACCESSION BC063885
VERSION BC063885.1 GI:39645656
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2949)
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AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Hunkeler, S.F., Zeng, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.O., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Vallal, D.K., Murray, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Maman, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 2949)

Strausberg, R.

Direct Submission

Submitted (08-DEC-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabs-x@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada

info@cgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabh, Parvaneh Saeedi, Jacqueline Schein, Duane Smal, Michael Smith, Lorraine Spence, Jeff Scott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAX Plate: 141 Row: Column: 21

This clone was selected for full length sequencing because it passed the following selection criteria: Genomescan gene prediction, similarity but not identity to protein.

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1..2949

Location/Qualifiers

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DEFINITION Sequence 4 from Patent WO03000903.
ACCESSION AX659639
VERSION AX659639.1 GI:29161819
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SOURCE Homo sapiens
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Xiao, Y.
TITLE Regulation of human nek-like serine/threonine protein kinase
JOURNAL Patent: WO 03000903-A 4 03-JAN-2003;
Bayer Aktiengesellschaft (DE)
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AX659636
LOCUS AX659636 1896 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 1 from Patent WO03000903.
ACCESSION AX659636
VERSION AX659636.1 GI:29161818
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Xiao Y.
TITLE Regulation of human nek-like serine/threonine protein kinase
JOURNAL Patent: WO 03000903-A 1 03-JAN-2003;
Bayer Aktiengesellschaft (DE)
FEATURES
Location/Qualifiers
source
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ORIGIN

Query Match 56.5%; Score 1338; DB 6; Length 1896;
Best Local Similarity 87.5%; Pred. No. 2.3e-302;
Matches 1553; Conservative 0; Mismatches 90; Indels 131; Gaps 3;
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Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A.,
Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K.,
Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y.,
Sekine,M., Kikuchi,H., Murakawa,K., Kanehori,K.,
Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
Sugano,S., Nagahara,K., Masuho,Y., Nagai,K. and Isogai,T.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 3635)
Isogai,T. and Yamamoto,J.
Direct Submission
Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; CDNA full insert sequencing;
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.

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Location/Qualifiers

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CDS

2712..3470

ORIGIN

Query Match 29.4%; Score 696.2; DB 9; Length 3635;
Best Local Similarity 98.6%; Pred. No. 4.4e-152;
Matches 712; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
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DB 1 CTTTITAGAGATCTTATTCCTCAATATTTGACTCTCTGAGGTCATTCAGGAAGATTCAG 60
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DB 61 TCACATGCTTATGTCAGAGCAGGAGCGCAGCTTCTGACATGCTGGAAAGGTGGTCCA 120
QY 902 GAAGTGTAAATACAAAAAGTCAGATTCGGGGAAGTCCACCAAGATCAAGGATATC 961
DB 121 GAAGTGTAAATACAAAAAGTCAGATTCAGGGAAGTCCACCAAGATCAAGGATATC 180
QY 962 TGTGCAATATAAGGAATGCTTATTCATAGAAATGAATGGAGACCACAGCTGGAGC 1021
DB 181 TGTGCAATATAAGGAATGCTTATTCATAGAAATGAATGGAGACCACAGCTGGAGC 240
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QY 1502 A 1502
DB 720 A 720

RESULT 12

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LOCUS Sequence 51 from Patent WO03000901.
DEFINITION AX803389
ACCESSION AX803389
VERSION AX803389.1 GI:38502052
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Martinez,R.A. and Sigurdsson,G.T.
TITLE Nucleic acids encoding protein kinases
JOURNAL Patent: WO 03000901-A 51 03-JAN-2003;
Decode Genetics EHP. (IS)

FEATURES

Location/Qualifiers

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ORIGIN

Query Match 25.4%; Score 602; DB 6; Length 1632;
Best Local Similarity 98.4%; Pred. No. 5.1e-130;
Matches 608; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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Db 801 TCCTGAGGTAAAGTTTGA 818

RESULT 13

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LOCUS Mus musculus expressed sequence BB049667, mRNA (CDNA clone
DEFINITION MGC:54821 IMAGE:6311513), complete cds.
ACCESSION BC053516
VERSION BC053516.1 GI:31565169
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 2281)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Heiton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 2281)
Strausberg, R.
Direct Submission
Submitted (09-JUN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
cDNA Library Preparation: ResGen, Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
Contact: nisc_mgc@nhgri.nih.gov
Web site: <http://www.nisc.nih.gov/>
Ahter, N., Avele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

REMARK
COMMENT

Through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAK Plate: 100 Row: d Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein.
Location/Qualifiers
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FEATURES
source

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ORIGIN

Query Match 25.2%; Score 597.4; DB 10; Length 2281;
Best Local Similarity 81.1%; Pred. No. 6.1e-129;
Matches 724; Conservative 0; Mismatches 156; Indels 13; Gaps 2;
QY 10 CCATGATAGTACGATGTGATTAGGCCATCGGCAAGTCCCTTCGGAAGCATACT 69
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QY 610 TTAAACATCTTTGAGGGTAACAATCTACGAGCTGGTCTGAAGATTTGTCAAGCAC 669
DB 664 TCAAGCATCTTTTGAAGACCAACATCTCCACCATCTGGTCTGAAGATTTGTCAAGGAC 723
QY 670 ATTTTGGCCCAATATCTCGGGGTTTCTCGTGGAGCTCCATTCCTTGATATCTCAGCTCT 729
DB 724 GTGTTGCTCCCATATCACCCACTTCTCTGAGACCTACAGTCTTGATACCTCAGCTCT 783
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QY 790 AGAATCTTATCCCAATATTTGATCTCTCTGAGTTC-ATTCAGGAGATTCAGTCAATG 848
DB 844 AATCTCTATTCCTCCGATCCCTTGTATCTCTGAGGCTCTGTTCAAGAGAAATCAGTCCACG 903
QY 849 CTTATATGACAGACGAGCGCCAGCTTCTCGACATGCTGGGAAGGTGGTCCA 901
DB 904 CTCACATGAGAACATGGCCATTTGGCCCCACAGCTTGTGGAGAGTTAGTCCA 956

RESULT 14

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DB 112 GAAAGATCTCGTGGTGGTTTGTACAGATTTCTCTAGGACTAAACATATTCATGACGG 171
QY 378 AAGATATTACACAGGACATAAAGCTCAGAACATTTTCTTAGCAAGAACGGAATGGTG 437
DB 172 AAGATATTACACAGGACATAAAGCTCAGAACATTTTCTTAGCAAGAACGGAATGGTG 231
QY 438 GCAAGCTTGGGACTTTGGTATAGCAAGAGTCTGAAATTAATTCATGGAATTTGTCGA 497
DB 232 GCAAGCTTGGGACTTTGGTATAGCAAGAGTCTGAAATTAATTCATGGAATTTGTCGA 272
QY 498 ACTTGATTGGAACACCTTACTACTCTGCCAGAGATCTGTGAGATTAACCCCTACAAC 557
DB 273 ----- 272
QY 558 AATAAAACGATATTTGGTCTTGGCTGTCTTATATGAGCTCTGCACATTAACAT 617
DB 273 -----GGATATTTGGTCTTGGCTGTCTTATATGAGCTCTGCACATTAACAT 324
QY 618 CCTTTTGAGGTAACACTTACAGAGCTGGTCTGAGGATTTGTCAAGCACATTTTGCC 677
DB 325 CCTTTTGAGGTAACACTTACAGAGCTGGTCTGAGGATTTGTCAAGCACATTTTGCC 384
QY 678 CCAATATCTCCGGGTTTCTCGTGGCTCCATTCCTTGATATCTCAGCTCTTCAAGTA 737
DB 385 CCAATATCTCCGGGTTTCTCGTGGCTCCATTCCTTGATATCTCAGCTCTTCAAGTA 444
QY 738 TCTCTCGAGACCGACATCCATAAATTCATTTTGAAGAGGCCCTTTTGAAGATCTT 797
DB 445 TCTCTCGAGACCGACATCCATAAATTCATTTTGAAGAGGCCCTTTTGAAGATCTT 504
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DB 505 ATTCCCAAAATATTTGACTCTCTGAG----- 528
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DB 529 ----- 528
QY 918 AAAGTGAATTCGCGGGAAGTCCCCCAAGATCAAGGATATCTGTGCCAATTAAGAG 977

ORIGIN

Query Match 24.3%; Score 576.2; DB 6; Length 1884;
Best Local Similarity 69.3%; Pred. No. 5.6e-124;
Matches 1017; Conservative 0; Mismatches 123; Indels 327; Gaps 4;
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RESULT 15

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BC068201 1745 bp mRNA linear PRI 31-MAR-2004
LOCUS BC068201 Homo sapiens cdna clone IMAGE:4771714, partial cds.
DEFINITION BC068201 Homo sapiens
ACCESSION BC068201.1 GI:45872598
VERSION BC068201.1
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1745)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

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Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Wokley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallos,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL PUBMED 12477932

2 (bases 1 to 1745)

Direct Submission

AUTHORS Strausberg,R.

TITLE

JOURNAL

REMARK

COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prabhu, Parvaneh Saeedi, JR Santos, Angeliue Schnerch, Ursula Skalska, Duane Smallos, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 51 Row: k Column: 4
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES

source

1. 1745
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4771714"
 /tissue type="Testis, embryonal carcinoma"
 /clone lib="NTH MGC_61"
 /lab host="DH10B"
 /note="Vector: pDNR-LIB"

ORIGIN

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 Best Local Similarity 66.0%; Pred. No. 1.5e-75;
 Matches 551; Conservative 0; Mismatches 281; Indels 3; Gaps 1;
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 Db 536 ATCATGGAGAGATGTTAGACTACAGAGATTGGAGAGGTTTCATTGGAAAGCCATT 595
 Qy 69 TTAGCTAAAGGGAATCATAGATGACGACCTGTGTCTATAAAGAGATCAATTTGAAAG 128

Db 596 CTGTGTTAAATCTACAGAAGATGGCAGACAGATATGTTATCAAGGAAATTAACATCTCAAGA 655
QY 129 ATGCCCATACAGAAAAAGAGCTTTCAAAGAAAGAGTATCTCTCGGAAAAAGATGAAA 188
Db 656 ATGTCAGTAAGAAAAAGAGAAATCAAGGAGAGAGAGTTCAGATATTCGCAAAACATGAAG 715
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QY 309 TTTAGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTTCTTAGGACTAAACATATT 368
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QY 369 CATGACAGGAAGATATTACAGGGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAAC 428
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QY 429 GGAATGGTGGCAACCTTGGGACCTTTGGTATAGCAAGAGTCCTGAATAATTCATGGAA 488
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Db 1193 TCTTTTCCACCTGTGCTCTTTCATTTATTCCTATGATCTCCGAGTTTGGTGTCTCAGTTA 1252
QY 729 TTTCAAGTATCTCCTCGAGACCGACCATCCATAAATTCATTTTGAAAAGGCCCTTTTATA 788
Db 1253 TTTAAAAGAAATCCTTAGGGATAGACCATCAGTCAACTCCATATTGGAGAAAGGTTTATA 1312
QY 789 GAGAACTTATTCCTCAAAATATTTGACTCCTGAGGTCATTGAGGAAGATTCAGTC 843
Db 1313 GCCAAACGATTTGAAAAGTTCTCTCTCTCAGCTTATTCAGAGAAATTTTGTC 1367

Search completed: November 8, 2004, 00:08:20
Job time : 9758 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2004, 19:19:58 ; Search time 1060 Seconds
(without alignments)
11736.913 Million cell updates/sec

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Perfect score: 2370
Sequence: 1 catggagaccatgataag.....ctgtcatgccgttacgagcg 2370

Scoring table: IDENTITY_NUC

Gapop 10_0, Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqn1990s.*
3: geneseqn2000s.*
4: geneseqn2001as.*
5: geneseqn2001bs.*
6: geneseqn2002as.*
7: geneseqn2002bs.*
8: geneseqn2003as.*
9: geneseqn2003bs.*
10: geneseqn2003cs.*
11: geneseqn2003ds.*
12: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1665	70.3	2240	6	ABK12426	Abk12426 Novel hum
3	1665	70.3	2816	12	ADJ96571	Adj96571 Human Nim
4	1656.2	69.9	1965	6	ABK12425	Abk12425 cDNA enco
5	1654	69.8	2052	6	ABK12424	Abk12424 cDNA enco
6	1449.4	61.2	1947	4	AAS06745	Aas06745 Polynucle
7	1349	56.9	1918	8	ABZ59717	Abz59717 Human NEX
8	1338	56.5	1896	8	ABZ59716	Abz59716 Human NOV
9	1199.6	50.6	1587	8	ABX72263	Abx72263 Human NOV
10	1176.8	49.7	1453	8	ABX72262	Abx72262 Human NOV
11	602	25.4	1632	10	ABZ77151	Abz77151 Human pro
12	597.4	25.2	1434	10	ADF44502	Adf44502 Mouse kin
13	597.4	25.2	2407	10	ADF44489	Adf44489 Mouse kin
14	369.4	15.6	4683	3	ABK13160	Abk13160 Human cDN
15	369.4	15.6	5426	5	AAS11582	Aas11582 Human cDN
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18	369.4	15.6	5448	9	ADB48336	Adb48336 Novel hum
19	369.4	15.6	5508	8	AAL51591	Aal51591 Human ser
20	369.4	15.6	5532	4	AAL58366	Aal58366 Human pol
21	369.4	15.6	5532	5	ADQ98575	Adq98575 DNA enco

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28	358.8	15.0	4263	3	AAA09328	Aaa09328 Human can
29	355.8	15.1	1588	8	ABX72261	Abx72261 Human NOV
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31	262.2	11.1	1781	8	ABX72260	Abx72260 Human NOV
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33	260.6	11.0	2257	8	ABX72259	Abx72259 Human NOV
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38	254.2	10.7	1991	12	ADI40889	Adi40889 Human kin
39	254.2	10.7	2050	10	ADC99119	Adc99119 Human KPP
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41	254.2	10.7	2110	6	AAD38850	Aad38850 Human kin
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44	254.2	10.7	3255	12	ADM16424	Adm16424 DNA enco
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ALIGNMENTS

RESULT 1
ABSS7149
ID ABSS7149 standard; cDNA; 2370 BP.
XX AC ABSS7149;
XX AC
DT 04-FEB-2003 (first entry)
XX DE Human cDNA encoding a serine/threonine kinase.
XX DE Human; ss; gene; serine/threonine kinase; lung carcinoma; chromosome 13.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 12..1934
XX FT /*tag= a
XX FT /product= "Ser/Thr kinase"
XX PN WO200281727-A2.
XX PD 17-OCT-2002.
XX PF 02-APR-2002; 2002WO-US010156.
XX PR 03-APR-2001; 2001US-00824583.
XX PR 05-JUN-2001; 2001US-00873404.
XX PA (PEKE) PE CORP NY.
XX PI Webster M, Yan C, Di Francesco V, Beasley EM;
XX DR WPI; 2003-058562/05.
XX DR P-PSDB; ABG72000.
XX PT Novel human kinase protein expressed in lung carcinoma and placenta is
XX PT useful to diagnose and treat diseases and disorders associated with
XX PT expression or activity of the protein.
XX PS Claim 22; Fig 1A; 101pp; English.
XX CC The invention relates to an isolated human kinase peptide of the
XX CC serine/threonine, an allelic variant or orthologue, and encoded by a
XX CC nucleic acid that hybridises under stringent conditions with the cDNA and

CC gene sequences appearing as ABS57149 and ABS57150, or a fragment
 CC comprising at least 10 contiguous amino acids. Also included are an
 CC antibody that selectively binds to the kinase, a gene chip comprising the
 CC nucleic acids, a transgenic non human animal comprising the nucleic
 CC acids, a nucleic acid vector comprising the nucleic acids, a host cell
 CC containing the vector and expressing the kinase, identifying a
 CC modulator/binding agent of the kinase (comprising contacting the peptide
 CC with an agent and determining if the agent has modulated function,
 CC expression or activity of the peptide or formed a complex with it). The
 CC molecules of the invention are useful to diagnose and treat a disorder
 CC characterised by aberrant expression of the protein (e.g. lung
 CC carcinoma). Agents which modulate the function or activity of the protein
 CC are useful to treat diseases or disorders mediated by human kinase
 CC protein. The gene for encoding the novel kinase is located on chromosome
 CC 13. The present sequence is the cDNA encoding the novel human kinase
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Query Match 100.0%; Score 2370; DB 8; Length 2370;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 661 GTCAAGCACATTTTGGCCCAATATCTCCGGGTTTCTCGTGAGCTCCATTCCTTGATAT 720
 Db 661 GTCAAGCACATTTTGGCCCAATATCTCCGGGTTTCTCGTGAGCTCCATTCCTTGATAT 720

Qy 721 CTCAGCTCTTTCAAGTATCTCTCGAGACCGAGCATCATAAATTCATTTGAAAAGGC 780
 Db 721 CTCAGCTCTTTCAAGTATCTCTCGAGACCGAGCATCATAAATTCATTTGAAAAGGC 780

781 CTTTTTAGAGAAATCTTATCCCAATATTTGACTCTCTGAGGTCAATTCAGGAAGATTC 840
 Db 781 CTTTTTAGAGAAATCTTATCCCAATATTTGACTCTCTGAGGTCAATTCAGGAAGATTC 840

Qy 841 GTCCATCTTATATGACAGAGGAGCGCCAGCTTCTCGACATGCTGGGAAGTGGTCC 900
 Db 841 GTCCATCTTATATGACAGAGGAGCGCCAGCTTCTCGACATGCTGGGAAGTGGTCC 900

Qy 901 AGAAGTGTAAATACAAAAGTGAATTCGGGGAAAGTCCCAAGATCAAGAGTAT 960
 Db 901 AGAAGTGTAAATACAAAAGTGAATTCGGGGAAAGTCCCAAGATCAAGAGTAT 960

Qy 961 CTGTGCCAATTAAGAGGAATGCTATATTTGATAGAAATGAATGAGACCAACAGCTGGAG 1020
 Db 961 CTGTGCCAATTAAGAGGAATGCTATATTTGATAGAAATGAATGAGACCAACAGCTGGAG 1020

Qy 1021 CCCAGAGCGCAGATCTATAAATATGATAAGAACCCCAAAATTTGCTGCTGTCTGGAC 1080
 Db 1021 CCCAGAGCGCAGATCTATAAATATGATAAGAACCCCAAAATTTGCTGCTGTCTGGAC 1080

Qy 1081 ATTATGATTTATTTATGCTCAACTTTGATATGCTGAGGAGAGAGCCCAAAACAAGTT 1140
 Db 1081 ATTATGATTTATTTATGCTCAACTTTGATATGCTGAGGAGAGAGCCCAAAACAAGTT 1140

Qy 1141 ATCCACCTTATTCCTCAAGAAAATCTGGAGTTGAGGATTACGGTCAGGAAACGAGGATG 1200
 Db 1141 ATCCACCTTATTCCTCAAGAAAATCTGGAGTTGAGGATTACGGTCAGGAAACGAGGATG 1200

Qy 1201 GTCCATCCCCAAGTCAATGGCTGCTGATACCTTCAGAGAAAATTTGAAGCTCAACAAT 1260
 Db 1201 GTCCATCCCCAAGTCAATGGCTGCTGATACCTTCAGAGAAAATTTGAAGCTCAACAAT 1260

Qy 1261 ATAAGTTCAAAAGTGGAGAGCAATTTGGTCTTCTGCTCATCTTCTGCGAGCCCAATTACA 1320
 Db 1261 ATAAGTTCAAAAGTGGAGAGCAATTTGGTCTTCTGCTCATCTTCTGCGAGCCCAATTACA 1320

Qy 1321 ACCAGAGCAAGAGCTTAAGAAAGTAAATGGAGAAAGCCCTAGATTCAGAGAGTGCATTTA 1380
 Db 1321 ACCAGAGCAAGAGCTTAAGAAAGTAAATGGAGAAAGCCCTAGATTCAGAGAGTGCATTTA 1380

Qy 1381 GGAAAAACGAATGAAGAACAGGAATATTGGAGAGCTTAGAGGAAATACGCCAACAGT 1440
 Db 1381 GGAAAAACGAATGAAGAACAGGAATATTGGAGAGCTTAGAGGAAATACGCCAACAGT 1440

Qy 1441 ACCTCAATGACATGAAGAAAATTAAGAAAGAGATGGGAGAGAACCCAGAGACATTGAAA 1500
 Db 1441 ACCTCAATGACATGAAGAAAATTAAGAAAGAGATGGGAGAGAACCCAGAGACATTGAAA 1500

Qy 1501 AAGACTTGAACAAATAGAGCTTCAGAACACAAAGGAAAGTAAATAATCCAGAACAGAAAT 1560
 Db 1501 AAGACTTGAACAAATAGAGCTTCAGAACACAAAGGAAAGTAAATAATCCAGAACAGAAAT 1560

Qy 1561 AATAAGCTTAAGAGGGGTAAATTTGAATTAATTTAGCAAAATGTATTTCTGATGAAA 1620
 Db 1561 AATAAGCTTAAGAGGGGTAAATTTGAATTAATTTAGCAAAATGTATTTCTGATGAAA 1620

Qy 1621 ACATCTCCCAAGAGGAAGAGCAATGGATATACCAATGAAACTTTGACCTTTGAGGATG 1680
 Db 1621 ACATCTCCCAAGAGGAAGAGCAATGGATATACCAATGAAACTTTGACCTTTGAGGATG 1680

Qy 1681 GCATGAAGTTTAAAGGAATATGAATGTGTAAGGAGCATGGGATTTATACAGACAAAGCAT 1740
 Db 1681 GCATGAAGTTTAAAGGAATATGAATGTGTAAGGAGCATGGGATTTATACAGACAAAGCAT 1740

Qy 1741 TTGAAAACTTCACTGCCAGAGCAGCATTTACAGAACTGACCTGGCTCAGTTTCTCTCT 1800
 Db 1741 TTGAAAACTTCACTGCCAGAGCAGCATTTACAGAACTGACCTGGCTCAGTTTCTCTCT 1800

Qy 1801 TCCTGGAAATCTCTGCTCATTTCTTCTGGAAAAATCTCCATTCAGCAGGACATCTTA 1860
 Db 1801 TCCTGGAAATCTCTGCTCATTTCTTCTGGAAAAATCTCCATTCAGCAGGACATCTTA 1860


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QY 841 GTCACATGCTTATATGACAGCAGGCGCCAGCTTCTCGACATGCTGGGAAGTGTGTC 900
Db 934 GTCACATGCTTATATGACAGCAGGCGCCAGCTTCTCGACATGCTGGGAAGTGTGTC 993
QY 901 AGAGTGTAATAACAAAGTGAAGATTCGCGGGAAGTGCACCAAGATCAAGATAT 960
Db 994 AGAGTGTAATAACAAAGTGAAGATTCGCGGGAAGTGCACCAAGATCAAGATAT 1053
QY 961 CTGTGCCAATTAAAGGAATGCTATATGCTATAGAAATGAATGAGACCAAGCTGAG 1020
Db 1054 CTGTGCCAATTAAAGGAATGCTATATGCTATAGAAATGAATGAGACCAAGCTGAG 1113
QY 1021 CCCAGAAGCCAGATCTATAAAATGATAGAAAGACCCAAATGCTGCTGTGTCGAC 1080
Db 1114 CCCAGAAGCCAGATCTATAAAATGATAGAAAGACCCAAATGCTGCTGTGTCGAC 1173
QY 1081 ATTATGATTATATATGCTCAACTTGATGCTGAGAGGAGAGCCCAAAACCAAGTT 1140
Db 1174 ATTATGATTATATATGCTCAACTTGATGCTGAGAGGAGAGCCCAAAACCAAGTT 1233
QY 1141 ATCACCTTATTCCTCAAGAAATATCTGAGTTGAGGATTAACGTCAGGAACAGGCGATG 1200
Db 1234 ATCACCTTATTCCTCAAGAAATATCTGAGTTGAGGATTAACGTCAGGAACAGGCGATG 1293
QY 1201 GTCCATCCCCAAGTCAATGGCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACAAT 1260
Db 1294 GTCCATCCCCAAGTCAATGGCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACAAT 1353
QY 1261 ATAGTTGAAGTGGAGNAGCAATGGTCTTCCTGCTCCATCTTCGCGAGCCCAATTA 1320
Db 1354 ATAGTTGAAGTGGAGNAGCAATGGTCTTCCTGCTCCATCTTCGCGAGCCCAATTA 1413
QY 1321 ACCAGAGCAAGAGCTAAGAAATTAAGAAAGATGGGAGAGACCTAGATTCAGAGAGCTGCAATTA 1380
Db 1414 ACCAGAGCAAGAGCTAAGAAATTAAGAAAGATGGGAGAGACCTAGATTCAGAGAGCTGCAATTA 1473
QY 1381 GGAAACGAAATGAGGAACAGAAATATGGAAGCAGTTAGAGGAATACGCAACAGT 1440
Db 1474 GGAAACGAAATGAGGAACAGAAATATGGAAGCAGTTAGAGGAATACGCAACAGT 1533
QY 1441 ACCTCAATGACATGAAGAAATTAAGAAAGATGGGAGAGACCAACAG----- 1488
Db 1534 ACCAATGACATGAAGAAATTAAGAAAGATGGGAGAGACCAACAGACTCAA 1593
QY 1489 ----- 1488
Db 1594 AAATAAGTCAATAAAACCTATTGTGTGAAGAGAGTAACCTGCTGTCATCAAGATGCAT 1653
QY 1489 -----AGCACATTGAAAAGACTTGAACAAATCAGGCTTCAGA 1527
Db 1554 CTGAGGGAAGACCTGTGAGAGCAATTTGAAAAGACTTGAACAAATCAGGCTTCAGA 1713
QY 1528 ACACAAAGGAAAGTAAATAACAGAACAGAAATATAAGCTTAAGAGGGGGTAAATTTG 1587
Db 1714 ACACAAAGGAAAGTAAATAACAGAACAGAAATATAAGCTTAAGAGGGGGTAAATTTG 1773
QY 1588 AAATTAATTTAGCAATATGTTTCTGATGAACATCTCTCCAGAGAGAGGCAATGG 1647
Db 1774 AAATTAATTTAGCAATATGTTTCTGATGAACATCTCTCCAGAGAGAGGCAATGG 1833
QY 1648 ATATACCAAAATGAAACTTTGACCTTTGAGGATGCGATGAAGTTTAAGGAATATGAATGTG 1707
Db 1834 ATATACCAAAATGAAACTTTGACCTTTGAGGATGCGATGAAGTTTAAGGAATATGAATGTG 1893
QY 1708 TAAAGGAGCATGGAGATTTACAGACAAAGCAATTTGAAAACTTCACTGCCAGAGAGCAG 1767
Db 1894 TAAAGGAGCATGGAGATTTACAGACAAAGCAATTTGAAAACTTCACTGCCAGAGAGCAG 1953
QY 1768 CATTTACAGAACTGACT 1784
Db 1954 GGTTTTCCAGCAGCT 1970
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RESULT 3
ADJ96571
ID ADJ96571 standard; DNA; 2816 BP.
XX
XX AC ADJ96571;
XX AC
XX DT 06-MAY-2004 (first entry)
XX
XX Human Nim-A related protein kinase NEK5 DNA SeqID 28.
DE
XX Gene; ds; kinase; human; tyrosine protein kinase;
KW serine/threonine protein kinase; PTK; STK; gene therapy; cancer;
KW immune-related disease; cardiovascular disease; brain;
KW neuronal associated disease; metabolic; inflammatory disorder;
KW cytosolic; neuroprotective; immunomodulator; antiinflammatory;
KW Nim-A related protein kinase; NEK5.
XX
XX Homo sapiens.
OS
XX 52.
XX WO2004006838-A2.
XX
XX 22-JAN-2004.
XX
XX 15-JUL-2003; 2003WO-US021730.
XX
XX 15-JUL-2002; 2002US-0395632P.
XX
XX (SUGEN-) SUGEN INC.
XX
XX Whyte D, Manning G, Caenepeel S;
XX
XX WPI; 2004-122753/12.
XX
XX P-PSDB; ADJ96637.
XX
XX New nucleic acid molecule encoding a kinase polypeptide, useful for
XX preparing a composition for treating diseases or disorders, e.g., cancer,
XX or neurological, immunological or inflammatory disorders.
XX
XX Example 1; SEQ ID NO 28; 366pp; English.
XX
XX This invention relates to a novel isolated, enriched or purified nucleic
XX acid molecule that encodes a kinase polypeptide. Specifically, it relates
XX to human tyrosine and serine/threonine protein kinases (PTK's and STK's),
XX as well as protein kinase-like enzymes. The present invention describes
XX screening methods to identify agonists, antagonists and antibodies that
XX can be used to modulate the activity or function of the mammalian kinase
XX enzymes. As such, these compositions can be used for gene therapy
XX purposes to treat diseases or disorders including cancer, immune-related
XX diseases, cardiovascular disease, brain or neuronal associated disease,
XX metabolic and inflammatory disorders. Accordingly, they exhibit
XX cytosolic, neuroprotective, immunomodulator and antiinflammatory
XX activities. This polynucleotide sequence is a human kinase DNA sequence
XX of the invention.
XX
XX Sequence 2816 BP; 977 A; 508 C; 675 G; 656 T; 0 U; 0 Other;
SQ
Query Match 70.3%; Score 1655; DB 12; Length 2816;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 10; Indels 93; Gaps 1;
QY 1 CATTGGAGACCATGGATTAAGTACGATGTGATTAAGGCCATCGGCAAGGTGCCCTTCGGGA 60
Db 307 CATTGGAGACCATGGATTAAGTACGATGTGATTAAGGCCATCGGCAAGGTGCCCTTCGGGA 366
QY 61 AAGCATCTAGCTTAAGGGAATCAGATACGACGACTGTGTCTATAAAGAGATCAATT 120
Db 367 AAGCATCTAGCTTAAGGGAATCAGATACGACGACTGTGTCTATAAAGAGATCAATT 426
QY 121 TTGAAAAGATGCCATACAGAAAAGAGCTTCAAGAAAAGAGTATCTTCTGAAA 180
Db 427 TTGAAAAGATGCCATACAGAAAAGAGCTTCAAGAAAAGAGTATCTTCTGAAA 486
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QY 181 AGATGAACATCCCAACATTGAGCTTCTTCAATTCATTTCAAGAGAAATGCGAGCTGT 240
Db 487 AGATGAACATCCCAACATTGAGCTTCTTCAATTCATTTCAAGAGAAATGCGAGCTGT 546
QY 241 TTAATGTAATGAATATTGTGATGAGGGGATCTCATGAAAGGATCAATAGACAAACGGG 300
Db 547 TTAATGTAATGAATATTGTGATGAGGGGATCTCATGAAAGGATCAATAGACAAACGGG 606
QY 301 GTGTGTTATTAGTGAAGATCAGATCCTCGGTGGTTGTACAGATTTCCTPAGACTAA 360
Db 607 GTGTGTTATTAGTGAAGATCAGATCCTCGGTGGTTGTACAGATTTCCTPAGACTAA 666
QY 361 ACATATTTCATGACAGAGAGATATACACAGGACATAAAAGCTCAGAACATTTTCTTA 420
Db 667 AACATATTTCATGACAGAGAGATATACACAGGACATAAAAGCTCAGAACATTTTCTTA 726
QY 421 GCAAGAACGGAATGGTGGCAAGCTTGGGACCTTTGGTATACAGAGTCCTGATATAT 480
Db 727 GCAAGAACGGAATGGTGGCAAGCTTGGGACCTTTGGTATACAGAGTCCTGATATAT 786
QY 481 CCATGGAACTTGCTCGAACTTGATTTGGAACACCTTACTACCTGTCCCCAGAGATCTGTC 540
Db 787 CCATGGAACTTGCTCGAACTTGATTTGGAACACCTTACTACCTGTCCCCAGAGATCTGTC 846
QY 541 AGAATAAACCCCTACACAAATAAACGGATATTGGTCTCTTGGCTGTCTTATATGAGC 600
Db 847 AGAATAAACCCCTACACAAATAAACGGATATTGGTCTCTTGGCTGTCTTATATGAGC 906
QY 601 TCTGCACACTTAAACATCCTTTGAGGGTAAACAACTTACAGAGCTGGTCTTGAAGATT 660
Db 907 TCTGCACACTTAAACATCCTTTGAGGGTAAACAACTTACAGAGCTGGTCTTGAAGATT 966
QY 661 GTCAAGCACATTTGGCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATAT 720
Db 967 GTCAAGCACATTTGGCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATAT 1026
QY 721 CTCAGCTCTTTCAAGTATCTCTCGAGACCGACCATCCATAAATCCATTTTGAAGAGC 780
Db 1027 CTCAGCTCTTTCAAGTATCTCTCGAGACCGACCATCCATAAATCCATTTTGAAGAGC 1086
QY 781 CTTTTTTAGAGAACTTTATCCCAATATTTGACCTCTGAGTCAATCAGGAAGAAATCA 840
Db 1087 CTTTTTTAGAGAACTTTATCCCAATATTTGACCTCTGAGTCAATCAGGAAGAAATCA 1146
QY 841 GTCAATGCTTATATGACAGACGAGCGCGAGCTTCTCGACATGCTGGGAGGTGTC 900
Db 1147 GTCAATGCTTATATGACAGACGAGCGCGAGCTTCTCGACATGCTGGGAGGTGTC 1206
QY 901 AGAAGTGTAATAACAAAAGTGAGATTCGGGGAAAGTGCCCAACCAAGATCAAGGATAT 960
Db 1207 AGAAGTGTAATAACAAAAGTGAGATTCAGGGAAAGTGCCCAACCAAGATCAAGGATAT 1266
QY 961 GTGTGCCAATTTAAAGGAATGCTATATGTCATAGAAATGAATGGAGACCAAGCTGGAG 1020
Db 1267 GTGTGCCAATTTAAAGGAATGCTATATGTCATAGAAATGAATGGAGACCAAGCTGGAG 1326
QY 1021 CCCAGAAGCCAGATCTATAAAATGATAGAAAGACCCAAATTCCTGCTGTGTGGAC 1080
Db 1327 CCCAGAAGCCAGATCTATAAAATGATAGAAAGACCCAAATTCCTGCTGTGTGGAC 1386
QY 1081 ATTATGATTTATTATGCTCAACTTGATATGCTGAGGAGAGAGCCCAACAAACCAAGTT 1140
Db 1387 ATTATGATTTATTATGCTCAACTTGATATGCTGAGGAGAGAGCCCAACAAACCAAGTT 1446
QY 1141 ATCACCCCTATTCTCAAGGAATATCTGGAGTTGAGGATTACGTCAGGAACGAGGCATG 1200
Db 1447 ATCACCCCTATTCTCAAGGAATATCTGGAGTTGAGGATTACGTCAGGAACGAGGCATG 1506
QY 1201 GTCCATCCCCAAGTCAATGGCTGTGAGTACCTTTAGAGAAATTTGAAGCTCAACAAAT 1260
Db 1507 GTCCATCCCCAAGTCAATGGCTGTGAGTACCTTTAGAGAAATTTGAAGCTCAACAAAT 1566
QY 1261 ATAAGTTGAAGTGAGAGAGCAATTTGGGTCTTCGTCCATCTCTGCGCGAGCAATTTACA 1320
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Db 1567 ATAAAGTTGAAAGTGGAGAGCAATTTGGGTCTTCTGTCATCTTCTGCGGACCAATTTACA 1626
QY 1321 ACCAGACACAGAGCTTAAGATTAATGGAGAGAGCTAGATTCCAGAGAGCTGCCATTTA 1380
Db 1527 ACCAGACACAGAGCTTAAGATTAATGGAGAGAGCTAGATTCCAGAGAGCTGCCATTTA 1686
QY 1381 GGAAGAAACGAAATGAAGAAACAGCAATATTGGAAAGCAGTTAGAGGAATACGCCAACAGT 1440
Db 1687 GGAAGAAACGAAATGAAGAAACAGCAATATTGGAAAGCAGTTAGAGGAATACGCCAACAGT 1746
QY 1441 ACCTCAATGACATGAAGAAATTTAGAAAGAAAGATGGGGAGAGAACCCAG----- 1488
Db 1747 ACCACATGACATGAAGAAATTTAGAAAGAAAGATGGGGAGAGAACCCAGAGAGAACTCAA 1806
QY 1489 ----- 1488
Db 1807 AAATAAGTCTATAAACCTTATTGGTGAAGAGAGTAACCTGCTGTCCATCAAGATGTCAT 1866
QY 1489 -----AGGACATTTGAAAAAGACCTTTGAAAAACAAATGAGGCTTTGAGA 1527
Db 1867 CTGAGGGAGAGACACCTGTGACGAGCAATTTGAAAAAGACTTTGAAAAACAAATGAGGCTTTGAGA 1926
QY 1528 ACACAAAGGAAAGTAAATAATCCAGACAGAAATATAAAGCTAAAGAGGGGTAAAAATTTG 1587
Db 1927 ACACAAAGGAAAGTAAATAATCCAGACAGAAATATAAAGCTAAAGAGGGGTAAAAATTTG 1986
QY 1588 AAATTAATTTAGACAAATGTATTTCTGATCAAAACATCTCTCCAAAGAGAGAGCAATGG 1647
Db 1987 AAATTAATTTAGACAAATGTATTTCTGATCAAAACATCTCTCCAAAGAGAGAGCAATGG 2046
QY 1648 ATATACCAATGAAACTTTGACCTTTGAGGATGGCATGAAATTTAAGGAATATGAATGTG 1707
Db 2047 ATATACCAATGAAACTTTGACCTTTGAGGATGGCATGAAATTTAAGGAATATGAATGTG 2106
QY 1708 TAAAGGAGCATGGAGATTATACAGACAAAGCAATTTGAAAAAATCTCACTGCCAGAGAGCAG 1767
Db 2107 TAAAGGAGCATGGAGATTATACAGACAAAGCAATTTGAAAAAATCTCACTGCCAGAGAGCAG 2166
QY 1768 CATTTACAGAACTGACT 1784
Db 2167 GGTTTTCCAGCAGACT 2183
RESULT 4
ABK12425
ID ABK12425 standard; cDNA; 1965 BP.
XX
AC ABK12425;
XX
AC AC
XX
DT 18-JUN-2002 (first entry)
XX
DE cDNA encoding novel human kinase protein #2.
XX
KW Novel human protein; NHP; serine-threonine kinase; brain;
KW calcium/calmodulin-dependent kinase; myosin light chain kinase;
KW biological disorder; spleen; placenta; chromosome 6; gene; ss.
XX
OS Homo sapiens.
XX
Key Key Location/Qualifiers
CDS 1..1965
FT /*tag= a
FT /product= "Human kinase protein #2"
XX
FN WO200218555-A2.
XX
PD 07-MAR-2002.
XX
PF 28-AUG-2001; 2001WO-US026776.
XX
PR 31-AUG-2000; 2000US-0229280P.
XX
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Db 1681 AAGTTTAAGGAATATGAATGTGTAAAGGAGCATGGAGATTATACAGACAAAGCAATTGAA 1740
Qy 1746 AAACCTTCACTGCCAGAGCAGCATTTTACAGAACTGACT 1784
Db 1741 AAACCTTCACTGCCAGAGCAGGTTTTCACGCGAGACT 1779

RESULT 5

ABK12424
ID ABK12424 standard; cDNA; 2052 BP.
XX

AC ABK12424;

DT 18-JUN-2002 (first entry)

XX cDNA encoding novel human kinase protein #1.

KW Novel human protein; NHP; serine-threonine kinase; brain;
KW calcium/calmodulin-dependent kinase; myosin light chain kinase;
KW biological disorder; spleen; placenta; chromosome 6; gene; ss.
XX

OS Homo sapiens.

XX Key Location/Qualifiers

FT 1. 2052
FT CDS /tag= a
FT /product= "Human kinase protein #1"

XX WO200218555-A2.

XX 07-MAR-2002.

XX 28-AUG-2001; 2001WO-US026776.

XX 31-AUG-2000; 2000US-0229280P.

XX (LEXI-) LEXICON GENETICS INC.

XX Fridele CJ, Hilbun E, Nepomnichy B, Hu Y;

XX WPI: 2002-292200/33.

XX P-PSDB; AAU77928.

PT Novel polynucleotide encoding novel human protein sharing structural
PT similarity with animal kinases e.g. serine-threonine, calcium/calmodulin-
PT dependent, and myosin light chain kinases, useful as probes and primers.
XX

PS Claim 1; Page 37-38; 46pp; English.

XX The present invention relates to the isolation of novel human proteins
CC (NHPs) and the polynucleotide sequences encoding them. The NHPs of the
CC invention are kinase proteins and share structural similarity to serine-
CC theonine, calcium/calmodulin-dependent, and myosin light chain kinases.
CC The sequences of the invention are useful for treating biological
CC disorders. The polynucleotide sequences encoding the kinase proteins can
CC be used as primers and probes. The sequences are also useful for
CC identifying mutations associated with a particular disease and also in a
CC prognostic or diagnostic assay. The present sequence encodes human
CC protein kinase #1 which is expressed in a broad range of human tissues
CC such as brain, spleen, and placenta. The gene encoding protein kinase #1
CC is located on chromosome 6

XX Sequence 2052 BP; 698 A; 388 C; 482 G; 484 T; 0 U; 0 Other;

Query Match 69.8%; Score 1654; DB 6; Length 2052;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 1763; Conservative 0; Mismatches 10; Indels 93; Gaps 1;

Qy 12 ATGATAAGTACGATGATTAAGCCATCGGCAAGTGCCTTCGGGAAAGCATCTTA 71

Db 1 ATGATAAGTACGATGATTAAGCCATCGGCAAGTGCCTTCGGGAAAGCATCTTA 60

Qy 72 GCTAAAGGGAATCAGATAGCAACGACTGTGTCTATAAAGAGATCAATTTTGAAGATG 131

Db 61 GCTAAAGGGAATCAGATAGCAACGACTGTGTCTATAAAGAGATCAATTTTGAAGATG 120
Qy 132 CCATACAGAAAAGAGAGCTTCAAGAAAAGAGTATCTTCTGGAAGAGTGAACAT 191
Db 121 CCATACAGAAAAGAGAGCTTCAAGAAAAGAGTATCTTCTGGAAGAGTGAACAT 180
Qy 192 CCACAACTTGTAGCTTCTTCAATTTCAATTTCAAGAGAATGGCAGGCTGTTTATTGTAATG 251
Db 181 CCACAACTTGTAGCTTCTTCAATTTCAATTTCAAGAGAATGGCAGGCTGTTTATTGTAATG 240
Qy 252 GAATATTGTGATGAGGGGATCTCATGAAGAAGATCAATAGACAACGGGGTGTGTTATTT 311
Db 241 GAATATTGTGATGAGGGGATCTCATGAAGAAGATCAATAGACAACGGGGTGTGTTATTT 300
Qy 312 AGTGAAGATCAGATCTCTCGGTTGTTGTACAGATTTCTCTAGACTATAAACAATATTCAT 371
Db 301 AGTGAAGATCAGATCTCTCGGTTGTTGTACAGATTTCTCTAGACTATAAACAATATTCAT 360
Qy 372 GACAGGAAGATATTACACAGGGACATAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 431
Db 361 GACAGGAAGATATTACACAGGGACATAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 420
Qy 432 ATGCTGCAAGCTTGTGTAACACCTTACTACTCTCCCGAGAGATCTGTCTAGATAAACC 551
Db 421 ATGCTGCAAGCTTGTGTAACACCTTACTACTCTCCCGAGAGATCTGTCTAGATAAACC 540
Qy 492 GCTCGAACTTGTATTGGAAACACCTTACTACTCTCCCGAGAGATCTGTCTAGATAAACC 551
Db 481 GCTCGAACTTGTATTGGAAACACCTTACTACTCTCCCGAGAGATCTGTCTAGATAAACC 540
Qy 552 TACAACAATAAAGCGGATATTGGTCTCTTGGCTGTCTTATATAGCTCTGCACACTT 611
Db 541 TACAACAATAAAGCGGATATTGGTCTCTTGGCTGTCTTATATAGCTCTGCACACTT 600
Qy 612 AAACATCTCTTTGAGGGTAACAACCTTACAGCAGCTGTTCTGAAGATTTGTCAAGCACAT 671
Db 601 AAACATCTCTTTGAGGGTAACAACCTTACAGCAGCTGTTCTGAAGATTTGTCAAGCACAT 660
Qy 672 TTGCCCCCAATATCTCCGGGTTTCTCGTAGCTCCATTCCTTTGATATCTCAGCTCTTT 731
Db 661 TTGCCCCCAATATCTCCGGGTTTCTCGTAGCTCCATTCCTTTGATATCTCAGCTCTTT 720
Qy 732 CAAGTATCTCTCGAGACCGACCATCCATAAATTCATTTTGAAGAGGCCCTTTTAGAG 791
Db 721 CAAGTATCTCTCGAGACCGACCATCCATAAATTCATTTTGAAGAGGCCCTTTTAGAG 780
Qy 792 AATCTTTATTTCCCAATATTGACTCTCTGAGTCAATTCAGAAAGAAATTCAGTCAATGCTT 851
Db 781 AATCTTTATTTCCCAATATTGACTCTCTGAGTCAATTCAGAAAGAAATTCAGTCAATGCTT 840
Qy 852 ATATGAGAGCAGGAGCGCCAGCTTCTGACATGCTGGGAAGGTGGTCCAGAAAGTATAA 911
Db 841 ATATGAGAGCAGGAGCGCCAGCTTCTGACATGCTGGGAAGGTGGTCCAGAAAGTATAA 900
Qy 912 ATACAAAAAGTCAGATTTCCGGGAAAGTCCCAAGATCAAGGATATCTGTGCCAAT 971
Db 901 ATACAAAAAGTCAGATTTCCAGGAAAGTCCCAAGATCAAGGATATCTGTGCCAAT 960
Qy 972 AAAGGAATGCTATATTGATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 1031
Db 961 AAAGGAATGCTATATTGATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 1020
Qy 1032 AGATCTATAAAAAATGATAGAAAAGCCAAAATTTGCTGTCTGTGGACATTTATGATTAT 1091
Db 1021 AGATCTATAAAAAATGATAGAAAAGCCAAAATTTGCTGTCTGTGGACATTTATGATTAT 1080
Qy 1092 TATTATGCTCAACTTGATATGCTGAGGAGGAGAGCCCAAAACCAAGTTATCACCTATT 1151
Db 1081 TATTATGCTCAACTTGATATGCTGAGGAGGAGAGCCCAAAACCAAGTTATCACCTATT 1140
Qy 1152 CTTCAAGAAATACCTGAGTTTACGCTCAGGAACCGAGCATGGTCCATCCCA 1211

Db 1141 CCTCAAGAAATACCTGGAGTTAGGATTACGGTCAGGAAACGAGGCATGTCATCCCA 1200
 QY 1212 AGTCATATGGCTCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAGTTGAAA 1271
 Db 1201 AGTCATATGGCTCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAGTTGAAA 1260
 QY 1272 GTGAGAGCAATTTGGTCTCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAGTTGAAA 1331
 Db 1261 GTGAGAGCAATTTGGTCTCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAGTTGAAA 1320
 QY 1332 GACCTAAGAGTAACTGAGAGAGCTTCAGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAGTTGAAA 1391
 Db 1321 GAGCTAAGAGTAACTGAGAGAGCTTCAGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAGTTGAAA 1380
 QY 1392 ATGAAGCAACAGGAATATTGGAAGAGCTTCAGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAGTTGAAA 1451
 Db 1381 ATGAAGCAACAGGAATATTGGAAGAGCTTCAGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAGTTGAAA 1440
 QY 1452 ATGAAGCAATTTAGAGAGAGCTTCAGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAGTTGAAA 1488
 Db 1441 ATGAAGCAATTTAGAGAGAGCTTCAGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAGTTGAAA 1500
 QY 1489 ----- 1488
 Db 1501 AAAACCTATTGTTGTAAGAGAGTAACCTGCTGTCATCAGATGCTATGAGGAGAA 1560
 QY 1489 -----AGGACATTGAAAGAGCTTGAACCAATAGAGCTTCAGAGCAACAAGGAA 1538
 Db 1561 GCACCTGTGAGGAGCATTGAAAGAGCTTGAACCAATAGAGCTTCAGAGCAACAAGGAA 1620
 QY 1539 AGTAAATATCCAGACAGAAATATAGCTTAAGCTTAAGAGGAGGTAATTTGAAATTAATTTA 1598
 Db 1621 AGTAAATATCCAGACAGAAATATAGCTTAAGCTTAAGAGGAGGTAATTTGAAATTAATTTA 1680
 QY 1599 GACAAATGTATTCTGATGAAACATCTCCAGAGAGAGAGCAATGGATATACCAAT 1658
 Db 1681 GACAAATGTATTCTGATGAAACATCTCCAGAGAGAGAGCAATGGATATACCAAT 1740
 QY 1659 GAACTTTGACCTTTGAGGATGGATGAGTTTAAAGATATCAATGTTAAAGGAGCAT 1718
 Db 1741 GAACTTTGACCTTTGAGGATGGATGAGTTTAAAGATATCAATGTTAAAGGAGCAT 1800
 QY 1719 GGAGATTATACAGACAAAGCATTTGAAAACTTCACTGCCAGAGAGCAGCATTTACAGAA 1778
 Db 1801 GGAGATTATACAGACAAAGCATTTGAAAACTTCACTGCCAGAGAGCAGCATTTACAGAA 1860
 QY 1779 CTGACT 1784
 Db 1861 CAGACT 1866

RESULT 6

AAS06745
 ID AAS06745 standard; cDNA; 1947 BP.

XX AC AAS06745;
 XX DT 12-SEP-2001 (first entry)

XX DE Polynucleotide sequence encoding human protein kinase #45.

XX KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
 KW metabolic disorder; immune related disease; neurological disorder;
 KW neurodegenerative disorder; inflammatory disorder; infectious disease;
 KW reproductive disorder; gene therapy; ss.

OS Homo sapiens.
 XX FN WO200138503-A2.
 XX PD 31-MAY-2001.
 XX PF 22-NOV-2000; 2000WO-US032085.

XX 24-NOV-1999; 99US-0167482P.
 PR (SUGEN-) SUGEN INC.
 PA Plowman GP, Whyte D, Manning G, Sudarsanam S, Martinez R;
 PI Flanagan P, Clary D;
 XX WPI; 2001-343950/36.
 DR P-PSDB; AAU03545.
 XX Nucleic acids encoding human kinase polypeptides, useful for preventing
 PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
 PT neuronal-associated diseases, and microbial infections.
 XX Example 1; Fig 1; 433pp; English.
 XX AAS06701-AAS06757 encode for novel human protein kinases #1-57. The novel
 CC protein kinases have been identified as members of the tyrosine or
 CC serine/threonine kinase (PTK and STK) families. The polynucleotides
 CC encoding protein kinases and the polypeptides may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC cancers (especially cancers of haematopoietic origin), cardiovascular
 CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
 CC immune related diseases (e.g. rheumatoid arthritis), neurological
 CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
 CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
 CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
 CC Additionally, polynucleotides encoding protein kinases may be used for
 CC gene therapy and as DNA probes in diagnostic assays. The protein kinase
 CC polypeptides may be used as antigens in the production of antibodies
 CC against the protein kinases and in assays to identify modulators of
 CC protein kinase expression and activity

XX Sequence 1947 BP; 638 A; 357 C; 455 G; 497 T; 0 U; 0 Other;

Query Match 61.2%; Score 1449.4; DB 4; Length 1947;
 Best Local Similarity 90.4%; Pred. No. 0;
 Matches 1602; Conservative 0; Mismatches 96; Indels 75; Gaps 2;

QY 12 ATGATAGTACGATGCTTAAAGCCATCGGCAAGTCCCTTCGGGAAGCATCTTA 71
 Db 1 ATGGATAGTACGATGCTTAAAGCCATCGGCAAGTCCCTTCGGGAAGCATCTTA 60
 QY 72 GCTAAGGGAATCAGATAGCAAGCTGTGTCTATAAAGAGATCAATTTGAAAAGATG 131
 Db 61 GCTAAGGGAATCAGATAGCAAGCTGTGTCTATAAAGAGATCAATTTGAAAAGATG 120
 QY 132 CCCATACAGAAAAAGAGCTTCAAGAAAGATGATGTTCTTCTGGAAGAGATGAACAT 191
 Db 121 CCCATACAGAAAAAGAGCTTCAAGAAAGATGATGTTCTTCTGGAAGAGATGAACAT 180
 QY 192 CCCACATTTAGCTTCTTCAATTTCAAGAGATGCGAGCTGTTTATTGTAATG 251
 Db 181 CCCACATTTAGCTTCTTCAATTTCAAGAGATGCGAGCTGTTTATTGTAATG 240
 QY 252 GAATATTGTGATGGAGGGGATCTCATGAAAAGATCAATAGACAAACCGGGTGTGTTATT 311
 Db 241 GAATATTGTGATGGAGGGGATCTCATGAAAAGATCAATAGACAAACCGGGTGTGTTATT 300
 QY 312 AGTGAAGATCAGATCTCGGTTGGTTGTACAGATTTCTCTAGGACTTAAACATATTTCAT 371
 Db 301 AGTGAAGATCAGATCTCGGTTGGTTGTACAGATTTCTCTAGGACTTAAACATATTTCAT 360
 QY 372 GACAGAGATATTACACAGGGACATAAAGCTCAGAACATTTTCTTAGCAAGACCGGA 431
 Db 361 GACAGAGATATTACACAGGGACATAAAGCTCAGAACATTTTCTTAGCAAGACCGGA 420
 QY 432 ATGGTGGCAAGCTTGGGACTTTGGTATAGCAAGCTCTGATATATTCATGGAACCTT 491
 Db 421 ATGGTGGCAAGCTTGGGACTTTGGTATAGCAAGCTCTGATATATTCATGGAACCTT 480

QY 492 GCTCGAACTTGTATTGGAACACCTTACTACTCTCTCCCGAGATCTGTCTCAGATAAACCC 551
DB 481 CTTCTGAACTTGTATTGGAACACCTTACTACTCTCTCCCGAGATCTGTCTCAGATAAACCC 540
QY 552 TACAACAATAAAACCGATTTTGGTCTCTTGGCTGTGTCTTATATAGCTCTGCAACATT 611
DB 541 TACAACAATAAAACCGATTTTGGTCTCTTGGCTGTGTCTTATATAGCTCTGCAACATT 600
QY 612 AAACATCTTTTTCAGGGTAAACACTTACAGCAGCTGGTCTCTGAGATTTTGTCAAGACAT 671
DB 601 AAACATCTTTTTCAGGGTAAACACTTACAGCAGCTGGTCTCTGAGATTTTGTCAAGACAT 660
QY 672 TTTGCCCAATATCTCCGGGTTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 731
DB 661 TTTGCCCAATATCTCCGGGTTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 720
QY 732 CRAATATCTCTCGAGACCGACCATCATTAATTCATTTTGAAGGCCCCCTTTTAGAG 791
DB 721 CAAGTATCTCTCGAGACCGACCATCATTAATTCATTTTGAAGGCCCCCTTTTAGAG 780
QY 792 AATCTTATTTCCCAATATTTGACTCTCTGAGGTCAATTCAGAGAAATTCAGTCACATGCTT 851
DB 781 AATCTTATTTCCCAATATTTGACTCTCTGAGGTCAATTTTGA----- 821
QY 852 ATATGACAGACGAGCGCCAGCTTCTCGACATGCTGGGAAGTGGTCCAGAAAGTGATAA 911
DB 822 -----GGTGACTGTTTGGATTTTGGCAGAGATTTTGGTTGCGAGTCCCTTG 867
QY 912 ATACAAAAAGTAGATTCGGGGAGAGTCCCAACCAAGATCAAGATATCTGTGCCAATT 971
DB 868 ACACGTGTGTTCGGTTTTAGTGTGAGCCACTGCACCCAGCTGTATTATGTTTTTAA 927
QY 972 AAAAGGAATGCTATATTTGATAGAAATGAATGGAGACCAACAGCTGGAGCCCAAGGCC 1031
DB 928 AACATCCCTCTGTTTTCTT----- 948
QY 1032 AGATCTATAAATATGATAGAACCCCAAAATGCTGCTGTCTGTGGACATTAATATAT 1091
DB 949 ----CAGATAAATATGATAGAACCCCAAAATGCTGCTGTGTGGACATTAATATAT 1005
QY 1092 TATTATGCTCACTTGTATGCTGAGGAGGAGCCCAACCAAGTTATCACCTATT 1151
DB 1006 TATTATGCTCACTTGTATGCTGAGGAGGAGCCCAACCAAGTTATCACCTATT 1065
QY 1152 CTTCAAGAAATACTGGAGTTGAGGATACGTTACGTTAGGAAACGAGGATGGTCCATCCCA 1211
DB 1066 CTTCAAGAAATACTGGAGTTGAGGATACGTTACGTTAGGAAACGAGGATGGTCCATCCCA 1125
QY 1212 AGTCAATGCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAAGTTGAA 1271
DB 1126 AGTCAATGCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAAGTTGAA 1185
QY 1272 GTGAGAAACAATTGGGTTCTTCTCATCTTCTGCGAGCCCAAAATTAACAACAGAGACAA 1331
DB 1186 GTGAGAAACAATTGGGTTCTTCTCATCTTCTGCGAGCCCAAAATTAACAACAGAGACAA 1245
QY 1332 GAGCTAAGAGTAATGGAAGAGCTAGATTCAGAGGCTGCCATTTAGGAAACCAAA 1391
DB 1246 GAGCTAAGAGTAATGGAAGAGCTAGATTCAGAGGCTGCCATTTAGGAAACCAAA 1305
QY 1392 ATCAAGGAAACAGGAATATTGGAAGCAGTTAGAGGAATACGCCAACAGTCACTCAATGAC 1451
DB 1306 ATCAAGGAAACAGGAATATTGGAAGCAGTTAGAGGAATACGCCAACAGTCACTCAATGAC 1365
QY 1452 ATGAAGAAATTTAGAAAGAGTGGGAGAGAACAGAGGACATTGAAAAAGACTTGAAA 1511
DB 1366 ATGAAGAAATTTAGAAAGAGTGGGAGAGAACAGAGGACATTGAAAAAGACTTGAAA 1425
QY 1512 CAATGAGCTTCAGAACCAAGGAAGTAAATATCCAGACAGAAATATAAGCTAAG 1571
DB 1426 CAATGAGCTTCAGAACCAAGGAAGTAAATATCCAGACAGAAATATAAGCTAAG 1485
QY 1572 AAGGGGTAAATTTGAAATTAATTTAGACAAATGTAATTTCTGTGAAAAACATCTCCAA 1631

DB 1486 AAGGGGTAAATTTGAAATTAATTTAGACAAATGTAATTTCTGTGAAAAACATCTCCAA 1545
QY 1632 GAGGAAGAGGCAATCGATATACCAATGAAACTTTGACCTTTGAGGATGGCATGAAGTTT 1691
DB 1546 GAGGAAGAGGCAATCGATATACCAATGAAACTTTGACCTTTGAGGATGGCATGAAGTTT 1605
QY 1692 AAGGAATATGAATGTGTAAGGAGCATGGAGATTTATACAGACAAAGCATTTGAAAACTT 1751
DB 1606 AAGGAATATGAATGTGTAAGGAGCATGGAGATTTATACAGACAAAGCATTTGAAAACTT 1665
QY 1752 CACTGCCCAGAGCAGCATTTTACAGAACTGACT 1784
DB 1666 CACTGCCCAGAGCAGGGTTTCCACGAGACT 1698

RESULT 7

ABZ59717
ID ABZ59717 standard; DNA; 1918 BP.

XX AC ABZ59717;

XX DT 17-APR-2003 (first entry)

XX DE Human NEK-like serine/threonine protein kinase DNA # SEQ ID 4.

XX KW Human; NEK-like serine/threonine protein kinase; cytostatic; cardiant;
antitumorigenic; nontoxic; neuroprotective; cancer; colon cancer;
cardiovascular disorder; diabetes; COPD; CNS disorder; ds.

XX OS Homo sapiens.

XX PN WO2003000903-A2.

XX PD 03-JAN-2003.

XX PF 24-JUN-2002; 2002WO-EP006948.

XX PR 25-JUN-2001; 2001US-0300068P.

XX PR 07-DEC-2001; 2001US-0336704P.

XX PA (FARB) BAYER AG.

XX PI Xiao Y;

XX WI WIPI; 2003-184051/18.

XX PT New polynucleotide encoding a NEK-like serine/threonine kinase
polypeptide useful for treating diseases associated with kinase
dysfunction, e.g. cardiovascular disorders, cancer such as colon cancer,
diabetes and CNS disorders.

XX PS Disclosure; Fig 4; 149pp; English.

XX CC The invention relates to a newly isolated polynucleotide encoding an NEK-
like serine/threonine protein kinase. The activity of the polynucleotide
and polypeptide of the invention may be described as cytostatic,
cardiant, antitumorigenic, nontoxic and neuroprotective. The expression
vector and reagent of the invention are useful for the preparation of a
medicament for modulating the activity of an NEK-like serine/threonine
kinase in a disease, such as cancer (e.g. colon cancer), cardiovascular
disorder, diabetes, COPD or CNS disorder. The polypeptides may also be
used to identify compounds which may act as activators or inhibitors at
the enzyme's active site, to raise specific antibodies which can block
the enzyme and effectively reduce its activity, as a bait protein in a
two-hybrid or three-hybrid assay to identify other proteins which bind to
or interact with the human NEK-like serine/threonine kinase polypeptide
and modulate its activity, and for the immunisation of mammals. The
current sequence represents human NEK-like serine/threonine protein
kinase encoding DNA

XX SQ Sequence 1918 BP; 615 A; 367 C; 460 G; 476 T; 0 U; 0 Other;

Query Match		56.9%; Score 1349; DB 8; Length 1918;
Best Local Similarity		87.6%; Pred. No. 0;
Matches 1564; Conservative		0; Mismatches 90; Indels 131; Gaps 3;
QY	1	CATTGGAGACCATGGTAAGTACCATGTGATTAAAGGCCATCGGGCAAGGTGCCTTCGGGA 60
DB	12	CATTGGAGACCATGGTAAGTACCATGTGATTAAAGGCCATCGGGCAAGGTGCCTTCGGGA 71
QY	61	AAGCATCTTACGTAAGGGAATCAGATAGCAAGCACTGTGTTCATATAAAGAGATCAATT 120
DB	72	AAGCATCTTACGTAAGGGAATCAGATAGCAAGCACTGTGTTCATATAAAGAGATCAATT 131
QY	121	TTGAAAGATCCCATCAAGAAAGAGAGCTTCAAGAAAGAGATGATCTTCTTGAAA 180
DB	132	TTGAAAGATCCCATCAAGAAAGAGAGCTTCAAGAAAGAGATGATCTTCTTGAAA 191
QY	181	AGATGAAACATCCCAACATTTAGCCTTCTTCAATTCATTTCAAGAAATGGCAGGCTGT 240
DB	192	AGATGAAACATCCCAACATTTAGCCTTCTTCAATTCATTTCAAGAAATGGCAGGCTGT 251
QY	241	TTATTGTAAGCAATTTGATCGAGGGATCTCATGAAAGGATCAATAGCAACGGG 300
DB	252	TTATTGTAAGCAATTTGATCGAGGGATCTCATGAAAGGATCAATAGCAACGGG 311
QY	301	CTGTGTTATTAGTCAAGATCAGATCCCTCGGTTGGTTTGTACAGATTCTCTAGGACTAA 360
DB	312	CTGTGTTATTAGTCAAGATCAGATCCCTCGGTTGGTTTGTACAGATTCTCTAGGACTAA 371
QY	361	AACATATTCTACAGGAAGATTTTACACAGGACATATAAGCTCAGAACATTTTCTTAA 420
DB	372	AACATATTCTACAGGAAGATTTTACACAGGACATATAAGCTCAGAACATTTTCTTAA 431
QY	421	GCAAGACGGAAATGGTGCAAGCTTGGGGACTTTGGTATAGCAAGAGTCTCTGAATAATT 480
DB	432	GCAAGACGGAAATGGTGCAAGCTTGGGGACTTTGGTATAGCAAGAGTCTCTGAATAATT 491
QY	481	CCATGGAACCTTCTGCAACATTTGGAACACCTTACTACCTGTCCCGCAGAGATCTGTC 540
DB	492	CCATGGAACCTTCTGCAACATTTGGAACACCTTACTACCTGTCCCGCAGAGATCTGTC 551
QY	541	AGATTAACCTTACACCAATATAAGGATTTTGGTCTCTTGGCTGTCTTATATGAGC 600
DB	552	AGATTAACCTTACACCAATATAAGGATTTTGGTCTCTTGGCTGTCTTATATGAGC 611
QY	601	TCTGCACACTTAAACATCTTTTGGGGTAAACAATTACAGCAGCTGGTTCTGAAGATT 660
DB	612	TCTGCACACTTAAACATCTTTTGGGGTAAACAATTACAGCAGCTGGTTCTGAAGATT 671
QY	661	GTCAGACATTTTGGCCCATATCTCGGGGTTTCTCGTAGCTCCATTCCTTGATAT 720
DB	672	GTCAGACATTTTGGCCCATATCTCGGGGTTTCTCGTAGCTCCATTCCTTGATAT 731
QY	721	CTCAGCTCTTCAAGTATCTCTCGAGACCGACCATCCATAAATTCATTTTGAAGGC 780
DB	732	CTCAGCTCTTCAAGTATCTCTCGAGACCGACCATCCATAAATTCATTTTGAAGGC 791
QY	781	CCTTTTATAGAAATCTTATCCCAATTTTGTACTCTCGAGCTCATTCAGGAAGATTC 840
DB	792	CCTTTTATAGAAATCTTATCCCAATTTTGTACTCTCGAGCTCATTCAGGAAGATTC 851
QY	841	GTCATGCTTATATGACAGAGAGGCGGCTTCTCGACATCTCGGGAAGTGTGTC 900
DB	852	GTCATGCTTATATGACAGAGAGGCGGCTTCTCGACATCTCGGGAAGTGTGTC 911
QY	901	AGAAGTGTAAATAACAAAAGTGAATTCGGGGAAAGTCCCGACCAAGATCAAGATAT 960
DB	912	AGAAGTGTAAATAACAAAAGTGAATTCGGGGAAAGTCCCGACCAAGATCAAGATAT 958
QY	961	CTGTGCCAATTAAGGAATGCTATTTGCTAGAGAAATGATGGAGA-CCACCAAGCTGGA 1019
DB	959	CTGTCTCTGAGGCTTTGACGGCTACAGCCCTGCGGCTGCTCTCACAGGCTGCTGTGAG 1018
QY	1020	GCCAGAGAGGCGAGATCTATAAATATAGAAAAGACCCAAAATTTGCTGCTGTGTGGA 1079
DB	1019	TGCTGCGGCTTTCCAGATATAAATATAGAAAAGACCCAAAATTTGCTGCTGTGTGGA 1078
QY	1080	CATTATGATTTATTTATGCTCAACTTGTATGCTGAGGAGAGAGCCCAAAACCAAGT 1139
DB	1079	CATTATGATTTATTTATGCTCAACTTGTATGCTGAGGAGAGAGCCCAAAACCAAGT 1138
QY	1140	TATCACCTTATTTCTCAAGAAATACCTGAGTTGAGGATTAACGTTCAAGAAACAGGAT 1199
DB	1139	TATCACCTTATTTCTCAAGAAATACCTGAGTTGAGGATTAACGTTCAAGAAACAGGAT 1198
QY	1200	GGTCCATCCCAAGTCAATGGCTGCTGAGTACCTTCAAGAAATTTGAAGCTCAACAA 1259
DB	1199	GGTCCATCCCAAGTCAATGGCTGCTGAGTACCTTCAAGAAATTTGAAGCTCAACAA 1258
QY	1260	TATTAAGTTGAAGTGAGAGCAATTTGGTCTTCTGCTCATCTTCTGCGGACCAATTTAC 1319
DB	1259	TATTAAGTTGAAGTGAGAGCAATTTGGTCTTCTGCTCATCTTCTGCGGACCAATTTAC 1284
QY	1320	AACACAGACACAGAGCTAAGAAATTAAGGAGAGAGCCCTAGATTCCAGGAGCTGCCATTT 1379
DB	1285	----- 1284
QY	1380	AGGAAACAGAAATGAAGAACAGAGCAATTTTGGAGCAGTTAGAGAAATACGCCACAG 1439
DB	1285	-----GGATATTGGAGCAGTTAGAGAAATACGCCACAG 1321
QY	1440	TACCTCAATGACATCAAAAGAAATTAAGAAAGATGGGAGAGAACACAGAGACATTGAA 1499
DB	1322	TACCAATGACATGAGAAATTAAGAAAGATGGGAGAGAACACAGAGACATTGAA 1381
QY	1500	AAAGACTTGAACCAATGAGCTTCAGAACCAAGAAAGATTAATAATCCAGAACAGAAA 1559
DB	1382	AAAGACTTGAACCAATGAGCTTCAGAACCAAGAAAGATTAATAATCCAGAACAGAAA 1441
QY	1560	TATAAGCTTAAGAGGGGTAAATTTGAAATTTAATTTAGACAAATGATTTCTGATGAA 1619
DB	1442	TATAAGCTTAAGAGGGGTAAATTTGAAATTTAATTTAGACAAATGATTTCTGATGAA 1501
QY	1620	AACATCTTCCAGAGAGAGCAATGATATACCAATGAACTTTGACCTTTGAGGAT 1679
DB	1502	AACATCTTCCAGAGAGAGCAATGATATACCAATGAACTTTGACCTTTGAGGAT 1561
QY	1680	GGCATGAAGTTTAAAGATATGATGTTAAAGGAGCATGGATTTATACAGAACAGCA 1739
DB	1562	GGCATGAAGTTTAAAGATATGATGTTAAAGGAGCATGGATTTATACAGAACAGCA 1621
QY	1740	TTTGAAGAACTTCACTGCGGAGAGCAGCATTTTACAGAACTGACT 1784
DB	1622	TTTGAAGAACTTCACTGCGGAGAGCAGGGTTTTCCAGCAGACT 1666
RESULT 8		
ABZ59716		
ID	ABZ59716	standard; DNA; 1896 BP.
XX	AC	ABZ59716;
XX	XX	
DT	17-APR-2003	(first entry)
XX	Human NEK-like serine/threonine protein kinase DNA # SEQ ID 1.	
DE	Human; NEK-like serine/threonine protein kinase; cytosolic; cardiac;	
KW	antiflammatory; neutropenic; neuroprotective; cancer; colon cancer;	
KW	cardiovascular disorder; diabetes; COPD; CNS disorder; gene; ds.	
XX	Homo sapiens.	
OS	XX	
XX	Key	Location/Qualifiers
PH	1..1896	
FT	CDs	
FT	/*tag= a	
FT	/product= "NEK-like serine/threonine protein kinase"	
XX	XX	

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PN WO2003000903-A2.
XX
XX 03-JAN-2003.
XX
XX 24-JUN-2002; 2002WO-EP006948.
XX
XX 25-JUN-2001; 2001US-0300068P.
XX PR 07-DEC-2001; 2001US-0336704P.
XX
XX (FARB ) BAYER AG.
XX
XX Xiao Y;
XX
XX WPI; 2003-184051/18.
XX DR P-PSDB; ABP71710.
XX
XX New polynucleotide encoding a NEK-like serine/threonine kinase
XX PT polypeptide useful for treating diseases associated with kinase
XX PT dysfunction, e.g. cardiovascular disorders, cancer such as colon cancer,
XX PT diabetes and CNS disorders.
XX
XX Claim 1 b; Fig 1; 149pp; English.
XX
XX The invention relates to a newly isolated polynucleotide encoding an NEK-
XX CC like serine/threonine protein kinase. The activity of the polynucleotide
XX CC and polypeptide of the invention may be described as cytostatic,
XX CC cardiant, antiinflammatory, nootropic and neuroprotective. The expression
XX CC vector and reagent of the invention are useful for the preparation of a
XX CC medicament for modulating the activity of an NEK-like serine/threonine
XX CC kinase in a disease, such as cancer (e.g. colon cancer), cardiovascular
XX CC disorder, diabetes, COPD or CNS disorder. The polypeptides may also be
XX CC used to identify compounds which may act as activators or inhibitors at
XX CC the enzyme's active site, to raise specific antibodies which can block
XX CC the enzyme and effectively reduce its activity, as a bait protein in a
XX CC two-hybrid or three-hybrid assay to identify other proteins which bind to
XX CC or interact with the human NEK-like serine/threonine kinase polypeptide
XX CC and modulate its activity, and for the immunisation of mammals. The
XX CC current sequence represents the human NEK-like serine/threonine protein
XX CC kinase encoding DNA
XX
XX Sequence 1896 BP; 608 A; 360 C; 455 G; 473 T; 0 U; 0 Other;
XX
XX Query Match 56.5%; Score 1338; DB 8; Length 1896;
XX Best Local Similarity 87.5%; Pred. No. 0;
XX Matches 1553; Conservative 0; Mismatches 90; Indels 131; Gaps 3;
XX
XX 12 ATGGATAAGTACGATGTGATTAAAGCCATCGGGCAAGTGCCTTCGGGAAAGCATACTTA 71
XX DB 1 ATGGATAAGTACGATGTGATTAAAGCCATCGGGCAAGTGCCTTCGGGAAAGCATACTTA 60
XX
XX 72 GCTAAAGGGAATCAGATAGCAAGCACTGTGTCTATAAAGAGATCAATTTTGAAGAAGTG 131
XX DB 61 GCTAAAGGGAATCAGATAGCAAGCACTGTGTCTATAAAGAGATCAATTTTGAAGAAGTG 120
XX
XX 132 CCATACAGAAAAAGAGCTTCAAGAAAGAGAGTATCTTCTGMAAAGATGAACAT 191
XX DB 121 CCATACAGAAAAAGAGCTTCAAGAAAGAGAGTATCTTCTGMAAAGATGAACAT 180
XX
XX 192 CCCAATGTAGCTTCTTCAATTCATTTCAAGAGAATGCGAGGCTGTTTATTGTATG 251
XX DB 181 CCCAATGTAGCTTCTTCAATTCATTTCAAGAGAATGCGAGGCTGTTTATTGTATG 240
XX
XX 252 GAATATGTGAGGGGATCTCATGAAGAGATCAATAGACACCGGGGTGTGTATTT 311
XX DB 241 GAATATGTGAGGGGATCTCATGAAGAGATCAATAGACACCGGGGTGTGTATTT 300
XX
XX 312 AGTGAAGATCAGATCCTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 371
XX DB 301 AGTGAAGATCAGATCCTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 360
XX
XX 372 GACAGAGATATTACACAGGACATATAAGCTCAGAACATTTTCTTAGCAAGACGGA 431
XX DB 361 GACAGAGATATTACACAGGACATATAAGCTCAGAACATTTTCTTAGCAAGACGGA 420
```


Db 388 GTGTGTTATTAGTGAAGATCAGATCCTCGTGTGTTTGTACAGATTCTCTAGCACTAA 447
Qy 361 AACATATTTCATGACAGGAAGATATTACACAGGACACATAAAAGCTCAGAACATTTTCTTA 420
Db 448 AACATATTTCATGACAGGAAGATATTACACAGGACACATAAAAGCTCAGAACATTTTCTTA 507
Qy 421 GCAGAACGGAATGTTGGGAAGCTTGGGAGCTTGGTATAGACAGAGTCTGAATAATT 480
Db 508 GCAAGAACGGAATGTTGGGAAGCTTGGGAGCTTGGTATAGACAGAGTCTGAATAATT 567
Qy 481 CCATGAACTTGTCTGCAACTTGTATTGGAACACCTTACTACCTGCTCCCGACAGAGATCTGC 540
Db 568 CCATGGAATCTTGTCTGCAACTTGTATTGGAACACCTTACTACCTGCTCCCGACAGATCTGC 627
Qy 541 AGAATAAACCCCTACAACTTAAAGGATATTGTTGTTCTTCTGCTGTGTTTATAGAGC 600
Db 628 AGAATAAACCCCTACAACTTAAAGGATATTGTTGTTCTTCTGCTGTGTTTATAGAGC 687
Qy 601 TCTGCACACTTAAACACTTCTTGGGTAAGCACTTACAGAGCTGTTCTGAGATTT 660
Db 688 TCTGCACACTTAAACACTTCTTGGGTAAGCACTTACAGAGCTGTTCTGAGATTT 747
Qy 661 GTCAAGCACATTTGCCCAATATCTCCGGGTTTCTCGTGTGAGTCCATTCCTTCAAT 720
Db 748 GTCAAGCACATTTGCCCAATATCTCCGGGTTTCTCGTGTGAGTCCATTCCTTCAAT 807
Qy 721 CTCAGCTCTTCAAGTATCTCTCGAGACCGACCATCCATAATTCATTTGAAAGGC 780
Db 808 CTCAGCTCTTCAAGTATCTCTCGAGACCGACCATCCATAATTCATTTGAAAGGC 867
Qy 781 CTTTTTAGAGATCTTATCCCAATATTTGACTCTCTGAGTCA--TTCAAGGAAGAT 837
Db 868 CTTTTTAGAGATCTTATCCCAATATTTGACTCTCTGAGTCA--TTGAGGAAGAT 927
Qy 838 TCAGTCACATGCTTATTCAGACAGGAGCGCCAGCTTCTCGAATGCTGGGAAGTGG 897
Db 928 TCAGTCACATGCTTATTCAGACAGGAGCGCCAGCTTCTCGAATGCTGGGAAGTGG 987
Qy 898 TCAGGAAGTGAATACAAAAGTGAATTCGGGGAAGTCCCAACCAAGATCAAGGA 957
Db 988 TCAGGAAGTGAATACAAAAGTGAATTCGGGGAAGTCCCAACCAAGATCAAGGA 1047
Qy 958 TATCTGTGCAATTAAGGAATGCTTATTCATAGAAATGAATGGAGACCAACAGCTG 1017
Db 1048 TATCTGTGCAATTAAGGAATGCTTATTCATAGAAATGAATGGAGACCAACAGCTG 1107
Qy 1018 GAGCCAGAGCGCAGATCTATAAAATGATAGAAAGCCCAAAATGCTGTCTGTG 1077
Db 1108 GAGCCAGAGCGCAGATCTATAAAATGATAGAAAGCCCAAAATGCTGTCTGTG 1167
Qy 1078 GACATTATGATTATTATGCTCAACTTGTATGCTGAGGAGAGCCCAACCA 1137
Db 1168 GACATTATGATTATTATGCTCAACTTGTATGCTGAGGAGAGCCCAACCA 1227
Qy 1138 GTTATCACCTATCTCAAGAAATACCTGGAGTTACGGTCAAGAAACAGGC 1197
Db 1228 GTTATCACCTATCTCAAGAAATACCTGGAGTTACGGTCAAGAAACAGGC 1287
Qy 1198 ATGGTCCATCCCAAGTCAATG 1219
Db 1288 ATGGTCCATCCCAAGTCAATG 1309

RESULT 10

ABX72262

ID ABX72262 standard; cDNA; 1453 BP.

XX AC ABX72262;

XX DT 03-JUN-2003 (first entry)

XX DE Human NOVX polynucleotide #93.

XX Human; NOVX; gene; ss; metabolic disorder; cardiomyopathy; diabetes; ASD;
KW hypertension; congenital heart defect; aortic stenosis; valve disease;
KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;
KW pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD;
KW tuberosus sclerosis; scleroderma; atherosclerosis; infectious disease;
KW obesity; anorexia; neurodegenerative disorder; Alzheimer's disease;
KW Parkinson's disease; immune disorder; haematopoietic disorder;
KW haemophilia; hypercoagulation; Crohn's disease; cancer.
OS Homo sapiens.
XX WO200281498-A2.
PN 17-OCT-2002.
XX 03-APR-2002; 2002WO-US010780.
PR 03-APR-2001; 2001US-0281086P.
PR 03-APR-2001; 2001US-0281136P.
PR 05-APR-2001; 2001US-0281883P.
PR 05-APR-2001; 2001US-0281906P.
PR 06-APR-2001; 2001US-0282020P.
PR 10-APR-2001; 2001US-0282930P.
PR 10-APR-2001; 2001US-0282934P.
PR 12-APR-2001; 2001US-0283512P.
PR 13-APR-2001; 2001US-0283710P.
PR 17-APR-2001; 2001US-0284234P.
PR 19-APR-2001; 2001US-0285325P.
PR 20-APR-2001; 2001US-0285381P.
PR 20-APR-2001; 2001US-0285609P.
PR 23-APR-2001; 2001US-0285748P.
PR 23-APR-2001; 2001US-0285890P.
PR 24-APR-2001; 2001US-0286088P.
PR 25-APR-2001; 2001US-0286292P.
PR 27-APR-2001; 2001US-0287213P.
PR 02-MAY-2001; 2001US-0288257P.
PR 29-MAY-2001; 2001US-0294164P.
PR 30-MAY-2001; 2001US-0294848P.
PR 18-JUN-2001; 2001US-0298952P.
PR 19-JUN-2001; 2001US-0299237P.
PR 19-JUN-2001; 2001US-0299276P.
PR 12-SEP-2001; 2001US-0318750P.
PR 25-SEP-2001; 2001US-0324800P.
PR 25-SEP-2001; 2001US-0324802P.
PR 27-SEP-2001; 2001US-0325684P.
PR 17-OCT-2001; 2001US-0330143P.
PR 14-NOV-2001; 2001US-0332131P.
PR 14-NOV-2001; 2001US-0332240P.
PR 21-NOV-2001; 2001US-0332779P.
PR 04-DEC-2001; 2001US-0332115P.
PR 03-JAN-2002; 2002US-0345783P.
PR 16-JAN-2002; 2002US-0350251P.
PR 02-APR-2002; 2002US-00114270.
(CURA-) CURAGEN CORP.

Guo X. Kekuda R. Miller CE, Malvankar UM, Spytek KA;
Patturajan M, Liu X, Gusev VV, Li L, Vernet CAM, Zerhusen BD;
Gorman L, Shenoy SG, Pena CE, Smithson G, Burgess CE, Gerlach V;
Padigaru M, Shinkets RA, Gangoli EA, Taupier RJ, Casman SJ, Ji W;
Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DU;
MacDougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA;
Ellerman K;

WPI; 2003-046858/04.

P-FSD; ABUS4634.

New isolated NOVX polypeptide useful for treating atherosclerosis,
metabolic disorders, diabetes, obesity, infectious disease, anorexia,
neurodegenerative disorders, Alzheimer's disease and cancer.

Claim 17; Page 291; 666pp; English.

The invention relates to human polypeptides, termed NOVX, and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for diagnosing disease, and screening for potential therapeutic agents. The sequences are useful for treating metabolic disorders, cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atrioventricular canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberculous sclerosis, scleroderma, atherosclerosis, obesity, infectious diseases, anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, immune disorders, haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease and cancer. Sequences ABX72170-ABX72275 represent human NOVX polynucleotides of the invention

Sequence 1453 BP; 466 A; 283 C; 309 G; 395 T; 0 U; 0 Other;

Query Match 49.7%; Score 1176.8; DB 8; Length 1453;

Best Local Similarity 99.1%; Pred. No. 9e-301;

Matches 1197; Conservative 0; Mismatches 2; Indels 9; Gaps 1;

QY	12	ATGGATAGTACGATGTGATTAAAGCCATCGGCAAGTGCCTTCGGGAAGCATACTTA	71
Db	1	ATGGATAGTACGATGTGATTAAAGCCATCGGCAAGTGCCTTCGGGAAGCATACTTA	60
QY	72	GCTAAAGGAAATCAGATAGCAAGCCTGTGTCATAAAGAGATCAATTTTGAAGATG	131
Db	61	GCTAAAGGAAATCAGATAGCAAGCCTGTGTCATAAAGAGATCAATTTTGAAG--	117
QY	132	CCCATACAGAAAGAGCTTCAAGAAAGAGTATCTTCGGAAGAGATGAACAT	191
Db	118	-----CAAGAAAGAGCTTCAAGAAAGAGTATCTTCGGAAGAGATGAACAT	171
QY	192	CCCAACATTTGAGCCTTCTCAATTCATTTCAAGAGAAATGCGAGCTGTGTTTGAATG	251
Db	172	CCCAACATTTGAGCCTTCTCAATTCATTTCAAGAGAAATGCGAGCTGTGTTTGAATG	231
QY	252	GAATATTGTGATGAGGGATCTCATGAAGAGATCAATAGCAACGGGTGTGTTATT	311
Db	232	GAATATTGTGATGAGGGATCTCATGAAGAGATCAATAGCAACGGGTGTGTTATT	291
QY	312	AGTGAAGATCAGATCCTCGGTGTTGTTACAGATTTCTTAGACTTAAACATATTCAT	371
Db	292	AGTGAAGATCAGATCCTCGGTGTTGTTACAGATTTCTTAGACTTAAACATATTCAT	351
QY	372	GACAGGAAGATATTACAGGGACATAAAGCTCAGAACATTTTCTTAGCAAGAACGGA	431
Db	352	GACAGGAAGATATTACAGGGACATAAAGCTCAGAACATTTTCTTAGCAAGAACGGA	411
QY	432	ATGTTGGCAAGCTTGGGACTTTGGTATAGCAAGATCCTGAATATTCATGGAACTT	491
Db	412	ATGTTGGCAAGCTTTGGGACTTTGGTATAGCAAGATCCTGAATATTCATGGAACTT	471
QY	492	GCTCGAATCTGTATTGGAAACCTTACTACTGTCCCGCAGAGATCTCTCAGAATAAACCC	551
Db	472	GCTCGAATCTGTATTGGAAACCTTACTACTGTCCCGCAGAGATCTCTCAGAATAAACCC	531
QY	552	TACAACTAAACGGATATTTGCTGCTGCTGCTGCTATATAGCTCTCCACACTT	611
Db	532	TACAACTAAACGGATATTTGCTGCTGCTGCTGCTATATAGCTCTCCACACTT	591
QY	612	AAACATCTCTTTTGAGGGTAAACATTTACAGAGCTGGTTCCTGAAGATTTGTCAGCACAT	671
Db	592	AAACATCTCTTTTGAGGGTAAACATTTACAGAGCTGGTTCCTGAAGATTTGTCAGCACAT	651
QY	672	TTTGCCCAATATCTCCGGGTTTTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT	731
Db	652	TTTGCCCAATATCTCCGGGTTTTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT	711
QY	732	CAAGTATCTCTCCGAGACCCAGCATTCATAAATTCATTTTGAAGGCCCTTTTAGAG	791
Db	712	CAAGTATCTCTCCGAGACCCAGCATTCATAAATTCATTTTGAAGGCCCTTTTAGAG	771

QY	792	AATCTTATTTCCAAATATTTGACTCTCTGAGGTCTATTGAGGAAGAAATTCAGTCACATGCTT	851
Db	772	AATCTTATTTCCAAATATTTGACTCTCTGAGGTCTATTGAGGAAGAAATTCAGTCACATGCTT	831
QY	852	ATATCCAGAGAGAGAGCCAGCTTCTCGACATGCTGGGAAGGTGGTCCAGAAAGTGTAAA	911
Db	832	ATATCCAGAGAGAGAGCCAGCTTCTCGACATGCTGGGAAGGTGGTCCAGAAAGTGTAAA	891
QY	912	ATACAAAAGTGAAGTTCGGGGAAGTCCCAACCAAGATCAAGATATCTGTGCCAATT	971
Db	892	ATACAAAAGTGAAGTTCGGGGAAGTTCAGGGAAGTCCCAACCAAGATCAAGATATCTGTGCCAATT	951
QY	972	AAAAGGAATGCTATATTCATATAGAAATGAATGGAGACACACAGCTGGAGGCCAGAGGCC	1031
Db	952	AAAAGGAATGCTATATTCATATAGAAATGAATGGAGACACACAGCTGGAGGCCAGAGGCC	1011
QY	1032	AGATCTATAAANAATGATAGAAAGCCCAAAATTTCTGCTGCTGTGGACATATTATGATTAT	1091
Db	1012	AGATCTATAAANAATGATAGAAAGCCCAAAATTTCTGCTGCTGTGGACATATTATGATTAT	1071
QY	1092	TATTATGCTCAACTTGTATATCTGAGGAGGAGAGCCCAAAACCAAGTTATCAACCCATT	1151
Db	1072	TATTATGCTCAACTTGTATATCTGAGGAGGAGAGCCCAAAACCAAGTTATCAACCCATT	1131
QY	1152	CCTCAAGAAATACCTGGAGTTGAGGATTACCGTCAGGNAACGAGGCATGTCATCCCA	1211
Db	1132	CCTCAAGAAATACCTGGAGTTGAGGATTACCGTCAGGNAACGAGGCATGTCATCCCA	1191
QY	1212	AGTCAATG 1219	
Db	1192	AGTCAATG 1199	

RESULT 11

ABZ77151

ID ABZ77151 standard; cDNA; 1632 BP.

AC ABZ77151;

XX 07-MAY-2003 (first entry)

DE Human protein kinase encoding cDNA SEQ ID NO:51.

Human; protein kinase; enzyme; antidiabetic; antiparkinsonian; antidiabetic; immunosuppressive; vulnary; gene therapy; COPD; asthma; migraine;

Chronic obstructive pulmonary disease; non-insulin dependent diabetes;

Parkinson's disease; myocardial infarction; inflammatory bowel disease;

autoimmune disorder; allograft rejection; inflammatory bowel disease;

cancer; leukaemia; wound granulation; gene; ss.

XX Homo sapiens.

Key Location/Qualifiers

CDS 1..1632

FT /*tag= a

FT /partial

FT /product= "protein kinase"

FT /note= "no start or stop codons given"

XX WO2003000901-A2.

XX 03-JAN-2003.

XX 24-JUN-2002; 2002WO-IB002358.

XX 26-JUN-2001; 2001US-0301098P.

XX 06-NOV-2001; 2001US-0332870P.

XX (DECO-) DECODE GENETICS EHF.

XX Martinez RAM, Sigurdsson GT;

```
XX WPI: 2003-201429/19.
DR P-PSDB; ABP96073.
XX
PT New protein kinase genes and polypeptides, useful for diagnosing diseases
PT associated with a protein kinase, or in gene therapy for treating e.g.
PT Parkinson's disease, migraine, myocardial infarction, allograft rejection
PT or cancers.
XX
XX Claim 1; Page 76; 258pp; English.
XX
XX ABZ77126 to ABZ77165 encode the human protein kinases given in ABP96048
XX to ABP96087. The protein kinases have antiasthmatic, antiinflammatory,
XX antidiabetic, antiparkinsonian, antimigraine, cardiant, cytostatic,
XX immunosuppressive and vulnary activities, and can be used in gene
XX therapy. A protein kinase therapeutic agent from the present invention,
XX particularly a protein kinase gene agonist or antagonist, can be used for
XX treating a disease or condition associated with a protein kinase in an
XX individual. These diseases include chronic obstructive pulmonary diseases
XX (COPD), asthma, non-insulin dependent diabetes, Parkinson's disease,
XX migraine, myocardial infarction, inflammatory bowel disease, autoimmune
XX disorders (e.g. allograft rejection or graft vs. host disease), cancers
XX (e.g. leukemias) or wound granulation
XX
XX Sequence 1632 BP; 459 A; 354 C; 415 G; 404 T; 0 U; 0 Other;
XX
XX Query Match 25.4%; Score 602; DB 10; Length 1632;
XX Best Local Similarity 98.4%; Pred. No. 1.6e-148;
XX Matches 608; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
XX
QY 215 TTCATTTCAAGAGATGGCAGCTGTTTATTTGTAATGGAATATTGTGATGAGGGGATCT 274
DB |||
QY 201 TTTTCTTACAGAGATGGCAGCTGTTTATTTGTAATGGAATATTGTGATGAGGGGATCT 260
DB |||
QY 275 CATGAAAAGGATCAATAGACACGGGGTGTGTTATTTAGTGAAGATCAGATCCCTCGGTG 334
DB |||
QY 261 CATGAAAAGGATCAATAGACACGGGGTGTGTTATTTAGTGAAGATCAGATCCCTCGGTG 320
DB |||
QY 335 GTTGTACAGATTTCTTAGGACTAAACATATTATCATGACAGGAAGATATTACACAGGGA 394
DB |||
QY 321 GTTGTACAGATTTCTTAGGACTAAACATATTATTCATGACAGGAAGATATTACACAGGGA 380
DB |||
QY 395 CATAAAAGCTCAGACATTTTCTTAGCAAGACGGATGTTGGCAAGCTTGGGGACTT 454
DB |||
QY 381 CATAAAAGCTCAGACATTTTCTTAGCAAGACGGATGTTGGCAAGCTTGGGGACTT 440
DB |||
QY 455 TGGTATAGCAAGAGCTTGAATAATTCCATGGAATTTGCTGAACTTGTATTGGAACACC 514
DB |||
QY 441 TGGTATAGCAAGAGCTTGAATAATTCCATGGAATTTGCTGAACTTGTATTGGAACACC 500
DB |||
QY 515 TTACTACCTGTCAGAGATCTGTGAGATTAACCCCTACACATAAAGCGATATTG 574
DB |||
QY 501 TTACTACCTGTCAGAGATCTGTGAGATTAACCCCTACACATAAAGCGATATTG 560
DB |||
QY 575 GTCTCTTGCTGTCTTATATGAGCTCTGCACACTTAAACATCTTTTGAGGGTAAACAA 634
DB |||
QY 561 GTCTCTTGCTGTCTTATATGAGCTCTGCACACTTAAACATCTTTTGAGGGTAAACAA 620
DB |||
QY 635 CTTACAGAGCTGTTGTTGAAGATTGCAAGCAATTTGCCCCCAATATCTCCGGGTT 694
DB |||
QY 621 CTTACAGAGCTGTTGTTGAAGATTGCAAGCAATTTGCCCCCAATATCTCCGGGTT 680
DB |||
QY 695 TTCTGTGAGCTCCATCTTCATATCTCAGCTCTTTCAAGTATCTCTCCGAGCCGACC 754
DB |||
QY 681 TTCTGTGAGCTCCATCTTCATATCTCAGCTCTTTCAAGTATCTCTCCGAGCCGACC 740
DB |||
QY 755 ATCCATAAATCCATTTTGAAGGCCCTTTTAGAGATCTTTATCCCAATATTTCAC 814
DB |||
QY 741 ATCCATAAATCCATTTTGAAGGCCCTTTTAGAGATCTTTATCCCAATATTTCAC 800
DB |||
QY 815 TCCTGAGTCATTCAGGA 832
DB |||
QY 801 TCCTGAGTGAAGTTTGA 818
DB |||
```

RESULT 12

ADP44502
ID ADP44502 standard; cDNA; 1434 BP.

XX AC ADP44502;

XX DT 12-FEB-2004 (first entry)

XX XX Mouse kinase protein encoding cDNA SEQ ID NO:20.

XX KW cytostatic; nootropic; neuroprotective; antidiabetic; screening;
XX KW regulation; drug development; protein-associated disease; cancer;
XX KW dementia; diabetes; kinase; enzyme; mouse; gene; ss.

XX OS Mus musculus.

XX XX WO2003084992-A1.

XX PN 16-OCT-2003.

XX PF 04-APR-2003; 2003WO-JP004330.

XX PR 05-APR-2002; 2002JP-00103396.

XX PR 23-APR-2002; 2002JP-00120904.

XX PR 02-MAY-2002; 2002JP-00130601.

XX PR 04-DEC-2002; 2002JP-00352520.

XX XX (RIKE) RIKEN KK.

XX PA (DNAF-) DNAFORM KK.

XX PA (MITU) MITSUBISHI CHEM CORP.

XX PI Hayashizaki Y, Kamiya M, Kubodera H, Watanabe W;

XX XX WPI: 2003-833568/77.

XX DR P-PSDB; ADP44528.

XX Proteins and encoded DNAs with kinase activity, useful in screening
XX substances for regulating such activity and in developing drugs for the
XX protein-associated diseases e.g. cancer, dementia and diabetes.

XX Claim 4; SEQ ID NO 20; 342pp; Japanese.

XX The present invention describes a protein: (a) containing any of the
XX amino acid sequences of ADP44509 to ADP44534 or ADP44544; or (b) based on
XX any of the sequences in (a) but with some amino acids deleted,
XX substituted and/or added and having kinase activity. Also described: (1)
XX a DNA encoding any of the proteins; (2) a full-length cDNA encoding the
XX protein; (3) a DNA which is: (a) a DNA containing any of the base
XX sequences in ADP44483 to ADP44508 or ADP44543; (b) a DNA derived from any
XX of the sequences in (a) but with some bases deleted; substituted and/or
XX added and encoding a protein with kinase activity; or (c) a DNA
XX hybridisable with any of the sequences in (a) or their complementary
XX strands under stringent conditions and encoding a protein with kinase
XX activity; (4) a recombinant vector containing the DNA; (5) a cell
XX transferred with the DNA or recombinant vector, or an individual produced
XX from the cell; (6) recombinant proteins produced by such cells; (7) an
XX oligonucleotide containing 5-10 consecutive bases in any of the base
XX sequences, its sense oligonucleotide, an antisense oligonucleotide with a
XX complementary strand of such sense oligonucleotide, or an oligonucleotide
XX derivative of the (anti-)sense oligonucleotide; (8) an antibody
XX specifically binding to the protein, or its partial fragment; (9) a
XX method for screening substances for regulating activity of the protein by
XX contacting a test substance with such protein before measuring changes in
XX the protein activity due to the test substance; (10) a method for
XX screening substances regulating expression of the DNA by contacting a
XX test substance with cells transfected with the gene and detecting changes
XX in expression level of the DNA in such cells; (11) recordable media for
XX reading in a computer with information on the amino acid sequences of the
XX proteins, and/or base sequences of the DNAs stored; and (12) a support
XX for binding with any of the proteins and/or DNAs. The proteins and their
XX encoded DNAs have cytostatic, nootropic, neuroprotective and antidiabetic

CC activities. They can be used in screening substances for regulating such
CC activity and in developing drugs for the protein-associated diseases e.g.
CC cancer, dementia and diabetes. The present sequence is used in the
XX exemplification of the present invention.

SQ Sequence 1434 BP; 392 A; 338 C; 336 G; 368 T; 0 U; 0 Other;

Query Match 25.2%; Score 597.4; DB 10; Length 1434;
Best Local Similarity 80.3%; Pred. No. 2.4e-147;
Matches 730; Conservative 0; Mismatches 166; Indels 13; Gaps 2;

```
QY 10 CCATGGATAAGTAGCATGTGATTAAGGCCATCGGCAAGGTGCTTCGGGAAAGCATACT 69
DB 102 CCATGGATAAATTTCACTGATTAAGATCATTTGGGAAGGACCTTTGGGAAGGTGACT 161
QY 70 TAGCTAAGGGAATCAGATAGCAGCACTGTGTCTATAAAGAGATCAATTTTGAAGA 129
DB 162 TGGCTAAGGATAAATCAGAAAGCAGTCACCTGTGTCTATAAAGAAATCAGTTTCAAG- 220
QY 130 TGCCCATACAGAAAGAAAGAGCTTCAAGAAAGAGTATTCTTCTGAAAGAGATGAAC 189
DB 221 -----GAAAAGAGGCTTCAAGAACAGTGTCTTCTGGCTAGATGGAGC 269
QY 190 ATCCCAATGTAGCTTCTTCAATTCATTTCAAGAGATGCGAGCTGTTTATTGTAA 249
DB 270 ATCCCAATATCGTAACCTTCTTCACTCGTTTCAAGAGAACGCGAGCTGTTTATTGTAA 329
QY 250 TGGAAATTTGTGAGGAGGATCTCATGAAAGAGATCAATAGACACGGGGTGTGTAT 309
DB 330 TGGAAATTTGTGAGGAGGATCTCATGAGAGATCCAGAGCGCGGGAGTGTAT 389
QY 310 TTAGTGAAGATCAGATCCTCGTGTGTTGTACAGATTTCTTAGGACTAAACATATTTC 369
DB 390 TCAGCAAGACCATCTGTGTGTGTTGTACAGATTTCTTAGGACTGAAGCATATTTC 449
QY 370 ATGACAGAGATATTACAGGAGACATAAAGCTCAGACATTTTCTTAGCAAGACG 429
DB 450 ATGACAGAGATTTTACAGGAGACATAAATCTCAGAAATATTTTCTTAGCAAGATG 509
QY 430 GAATGCTGGCAAGCTTGGGACCTTTGGTATAGCAAGAGTCTTCAATATTCATGGAAC 489
DB 510 GAATGTTGCCAAGCTCGGGACCTTTGCAACAGCAAGCACTGAATGACTCCATGGAAC 569
QY 490 TTGCTCGAATTTGTAACACCTTACTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 549
DB 570 TTGCTCAACATGTGCTGGGACCTTACTACCTGCTGCTGCTGCTGCTGCTGCTGCTG 629
QY 550 CCTCAACAATAAAGAGATTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 609
DB 630 CATCAACAATAAAGAGATCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 689
QY 610 TTAACATCTCTTTGAGGATTAACATTTACAGAGCTGGTCTGGAAGATTTGTCAGAC 669
DB 690 TCAAGCATCTCTTTGAGAGCAACAATCTCACCACCTGTTCTGGAAGATTTGTCAGAG 749
QY 670 ATTTTGGCCCAATCTCCGGGGTTTTCTCGTGAGCTCCATCTCTGATATCTCAGTCT 729
DB 750 GTGTTGCTCCATATACCCCACTTCTCTGTAACCTACAGTCTTGTATACCTCAGCTCT 809
QY 730 TTCAAGTATCTCTCGAGACCGACCATCCATAAATTCATTTTGAAGAGCCCTTTTATG 789
DB 810 TCAGAGTGTCTCTCAGACCGGCACTCCGTAGTCCCTTTTGAAGAGCCCTTTTATG 869
QY 790 AGAATCTTATCCCAATATTGACTCTCTGAGTCTC-ATTCAGAGAGATTCAGTCAATG 848
DB 870 AACTCTCATTTGCTCCGATCTTGTATCTGAGGTCTGTTCAAGAGAGATCCAGTCCACG 929
QY 849 CTTATATGCAAGCAGGAGCGCCAGCTTCTCGACATGCTGGGAGGTGTGTCAGAGATGT 908
DB 930 CTCACATGGAGAACATGCCATTGGCCCCACAGCTTGTTCGAGAGTTAGTCCATGTGGG 989
QY 909 AANATCAA 917
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Db 990 ATCATGTAA 998

RESULT 13
ADP44489
ID ADF44489 standard; cDNA; 2407 BP.

XX AC ADF44489;
XX DT 12-FEB-2004 (first entry)
XX Mouse kinase protein encoding cDNA SEQ ID NO:7.

DE cytotatic; nootropic; neuroprotective; antidiabetic; screening;
KW regulation; drug development; protein-associated disease; cancer;
KW dementia; diabetes; kinase; enzyme; mouse; gene; ss.
XX Mus musculus.
XX WO2003084992-A1.
XX 16-OCT-2003.
XX 04-APR-2003; 2003WO-JP004330.
XX 05-APR-2002; 2002JP-00103396.
PR 23-APR-2002; 2002JP-00120904.
PR 02-MAY-2002; 2002JP-00130601.
PR 04-DEC-2002; 2002JP-00352520.
XX (RIKE) RIKEN KK.
XX PA (DNAP-) DNAFORM KK.
XX PA (MITU) MITSUBISHI CHEM CORP.
XX Hayashizaki Y, Kamiya M, Kubodera H, Watanabe W;
XX WPI; 2003-833568/77.
DR P-PSDB; ADF44515.

XX Proteins and encoded DNAs with kinase activity, useful in screening
substances for regulating such activity and in developing drugs for the
protein-associated diseases e.g. cancer, dementia and diabetes.

PS Claim 4; SEQ ID NO 7; 342bp; Japanese.

CC The present invention describes a protein: (a) containing any of the
CC amino acid sequences of ADF44509 to ADF44534 or ADF44544; or (b) based on
CC any of the sequences in (a) but with some amino acids deleted,
CC substituted and/or added and having kinase activity. Also described: (1)
CC a DNA encoding any of the proteins; (2) a full-length cDNA encoding the
CC protein; (3) a DNA which is: (a) a DNA containing any of the base
CC sequences in ADF4483 to ADF44508 or ADF44543; (b) a DNA derived from any
CC of the sequences in (a) but with some bases deleted, substituted and/or
CC hybridisable with any of the sequences in (a) or their complementary
CC strands under stringent conditions and encoding a protein with kinase
CC activity; (4) a recombinant vector containing the DNA; (5) a cell
CC transfected with the DNA or recombinant vector, or an individual produced
CC from the cell; (6) recombinant proteins produced by such cells; (7) an
CC oligonucleotide containing 5-10 consecutive bases in any of the base
CC sequences, its sense oligonucleotide, an antisense oligonucleotide with a
CC complementary strand of such sense oligonucleotide, or an oligonucleotide
CC derivative of the (anti-)sense oligonucleotide; (8) an antibody
CC specifically binding to the protein, or its partial fragment; (9) a
CC method for screening substances for regulating activity of the protein by
CC contacting a test substance with such protein before measuring changes in
CC the protein activity due to the test substance; (10) a method for
CC screening substances regulating expression of the DNA by contacting a
CC test substance with cells transfected with the gene and detecting changes
CC in expression level of the DNA in such cells; (11) recordable media for
CC reading in a computer with information on the amino acid sequences of the
CC proteins, and/or base sequences of the DNAs stored; and (12) a support
CC for binding with any of the proteins and/or DNAs. The proteins and their

CC encoded DNAs have cytostatic, neurotropic, neuroprotective and antidiabetic
 CC activities. They can be used in screening substances for regulating such
 CC activity and in developing drugs for the protein-associated diseases e.g.
 CC cancer, dementia and diabetes. The present sequence is used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 2407 BP; 718 A; 528 C; 604 G; 557 T; 0 U; 0 Other;

Query Match 25.2%; Score 597.4; DB 10; Length 2407;
 Best Local Similarity 81.1%; Pred. No. 3.1e-147;
 Matches 724; Conservative 0; Mismatches 156; Indels 13; Gaps 2;
 QY 10 CCATGTAAGTACGATGATTAAGGCCATCGGCAAGTCCCTTCGGGAAGCATACT 69
 DB 90 CCATGTAAGTACGATGATTAAGGCCATCGGCAAGTCCCTTCGGGAAGTACT 149
 QY 70 TAGCTAAGGGAAATCAGATAGACGACTGTGTATTAAGAGATCAATTTTGAAGA 129
 DB 150 TGGCTAAGGAAATCAGATAGACGACTGTGTATTAAGAGATCAATTTTGAAGA 208
 QY 130 TGCCCATACAAGAAAAGAGCTTCAAGAAAAGAGTATCTTCTGGAAGAGATGAAC 189
 DB 209 -----GAAAAGAGGCTCAAGAGAGAGTATCTTCTGCTAGGATGGAGC 257
 QY 190 ATCCCAACATGTAGCTTCTTCAATTCATTTCAAGAGATGGCAGGCTGTATTGTA 249
 DB 258 ATCCCAATATCGTAACCTTCTTCAAGAGAGAGTATCTTCTGCTAGGATGGAGC 317
 QY 250 TGGATATTGTATGGGGGATCTCATGAAGAGATCAATAGACACGGGGTGTATT 309
 DB 318 TGAATACTGTATGGGGGATCTCATGAAGAGATCAATAGACACGGGGTGTATT 377
 QY 310 TTAGTGAAGATCAGATCTCTGGTGTGTATGAGATTTCTTAGGACTAAACATATTC 369
 DB 378 TCAGGAGAGACAGATCTCTGGTGTGTATGAGATTTCTTAGGACTAAACATATTC 437
 QY 370 ATGACAGGAGATATATACAGGAGATCAATAGAGATCAATAGACACGGGGTGTATT 429
 DB 438 ATGACAGGAGATATATACAGGAGATCAATAGAGATCAATAGACACGGGGTGTATT 497
 QY 430 GAATGTGCAAGCTTGGGAGCTTGGTATAGAGAGTCTGATATATTCATGGAGAC 489
 DB 498 GAATGTGCAAGCTTGGGAGCTTGGTATAGAGAGTCTGATATATTCATGGAGAC 557
 QY 490 TTGCTGCAATGTATGTAAACACTTACTACTGCTCCAGAGATCTGTAGATATAAC 549
 DB 558 TTGCTCAAAACATGTGCTGGGACACTTACTACTGCTCCAGAGATCTGTAGATATAAC 617
 QY 550 CCTACACATATAACCGGATATTTGGTCTCTTGGCTGTCTTATATGAGCTCTGCAC 609
 DB 618 CATACACATATAACCGGATATTTGGTCTCTTGGCTGTCTTATATGAGCTCTGCAC 677
 QY 610 TTAACATCTTTTGAAGGTAACACTTACAGAGCTGTTCTGAAGATTTGTCAAGCAC 669
 DB 678 TCAAGCATCTTTTGAAGGTAACACTTACAGAGCTGTTCTGAAGATTTGTCAAGCAC 737
 QY 670 ATTTGCCCCATATCTCCGGGTTTCTGCTGAGCTCCATCTTGTATCTCAGCTCT 729
 DB 738 GTGTTGCTCCCATATCACCCTTCTCTGCTGAGCTCCATCTTGTATCTCAGCTCT 797
 QY 730 TTCAAGTATCTCTCGAGACCGACCATCCATAAATTTCAATTTGAAAAGGCCCTTTTAG 789
 DB 798 TCAGAGTGTCTCTCAGACCGGCAATCGTTACGCTCCCTTTGAAAAGGCCCTTTTAG 857
 QY 790 AGATCTTATTTCCAAATATTTGACTCTCAGGCTC-ATTTCAGAGAGATTCAGTCAATG 848
 DB 858 AAACCTCTATTGCCCCATCTTGTATCTGAGTCTGTTTCAAGAGAGATTCAGTCCCCAG 917
 QY 849-CTTATATGAGAGAGAGCGGCGGCTTCTCGACATGCTGGGAAGTGTCCA 901
 DB 918 CTCACATGAGAGAGATGCGCATTTGGCCCAACAGCTTGTGGAGAGTAGTCCA 970

RESULT 14
 ABX13160
 ID ABX13160 standard; cDNA; 4683 BP.
 XX AC ABX13160;
 DT 10-MAY-2003 (first entry)
 XX Human cDNA for kinase and phosphatase, KPP-14, INCYTE No. 8043337CBI.
 DE Human; ss; gene; kinase and phosphatase; KPP; cancer; cirrhosis;
 XX cell proliferative disorder; arteriosclerosis; atherosclerosis;
 KW hepatitis; paroxysmal nocturnal haemoglobinuria; polycythaemia vera;
 KW psoriasis; primary thrombocytopaenia; developmental disorder;
 KW renal tubular acidosis; anaemia; mental retardation; AIDS; epilepsy;
 KW neurological disorder; Alzheimer's disease; Parkinson's disease;
 KW autoimmune disorder; inflammatory disorder; allergy; asthma;
 KW acquired immunodeficiency syndrome; autoimmune thyroiditis;
 KW contact dermatitis; Crohn's disease; diabetes mellitus;
 KW glomerulonephritis; Goodpasture's syndrome; gout; Graves' disease;
 KW Hashimoto's thyroiditis; irritable bowel syndrome; multiple sclerosis;
 KW osteoarthritis; osteoporosis; pancreatitis; Reiter's syndrome;
 KW rheumatoid arthritis; Sjogren's syndrome; uveitis; infection.
 XX Homo sapiens.
 OS WO2003012065-A2.
 XX 13-FEB-2003.
 XX 01-AUG-2002; 2002WO-US024521.
 XX 02-AUG-2001; 2001US-0309627P.
 PR 07-AUG-2001; 2001US-0310933P.
 PR 09-AUG-2001; 2001US-0311323P.
 PR 07-SEP-2001; 2001US-0317820P.
 PR 14-SEP-2001; 2001US-0322264P.
 PR 28-SEP-2001; 2001US-0326098P.
 PR 19-DEC-2001; 2001US-0343007P.
 PR 15-MAR-2002; 2002US-036494P.
 PR 24-APR-2002; 2002US-0375539P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX Baughn MR, Yue H, Walia NK, He A, Au-Young JK, Lee SY;
 PI Gietzen KJ, Lal PG, Elliott VS, Ison CH, Yang J, Lee BA, Li JX;
 PI Emerling BM, Richardson TW, Warren BA, Hafalia AJA, Marquis JP;
 WPI: 2003-239519/23.
 P-PSDB, ABU08113.
 PT New human kinases and phosphatases and polynucleotides, useful for
 diagnosing, treating or preventing autoimmune or inflammatory disorders
 (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
 cancer or hepatitis.
 XX Claim 5; Page 194-196; 199pp; English.
 PS The invention relates to an isolated polypeptide, which is a human kinase
 and phosphatase, KPP (KPP-1 to KPP-18). Also included are the encoding
 polynucleotides KPP NA, recombinant polynucleotide comprising a promoter
 sequence operably linked to KPP NA, a cell transformed with the
 recombinant polynucleotide, a transgenic organism comprising the
 recombinant polynucleotide, an anti-KPP antibody, screening for
 anti-agonists of KPP, screening for compounds which bind to or alter the
 activity or expression of KPP, microarray where at least one element is
 KPP NA, generating an expression profile of a sample containing
 polynucleotides and an array comprising different nucleotide molecules
 affixed in distinct physical locations on a solid substrate (where at
 least one of the nucleotide molecules comprises a first oligonucleotide
 or polynucleotide sequence specifically hybridisable with at least 30
 contiguous nucleotides of a target KPP NA). The kinases and phosphatases
 (KPP) polypeptides, polynucleotides, agonists and antagonists are useful

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2004, 21:19:48 ; Search time 219 Seconds
(without alignments)
7692.099 Million cell updates/sec

Title: US-10-730-010-1

Perfect score: 2370

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Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2370	100.0	2370	4	US-09-873-404-1
2	2370	100.0	2370	4	US-10-243-735-1
3	369.4	15.6	5448	4	US-09-620-312D-246
4	369.4	15.6	5532	4	US-09-620-312D-245
5	355.8	15.0	4263	4	US-09-166-350-29
6	238.4	10.1	1846	3	US-09-173-581-15
7	238.4	10.1	1846	3	US-09-420-915-15
8	205.2	8.7	63588	4	US-09-873-404-3
9	205.2	8.7	63588	4	US-10-243-735-3
10	170.2	7.2	2079	4	US-09-992-481-1
11	166.8	7.0	2940	3	US-08-870-529-1
12	166.8	7.0	2940	3	US-09-544-794-1
13	166.8	7.0	3264	3	US-08-870-529-8
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16	131.6	5.6	1938	4	US-10-196-927-1
17	131.6	5.6	2847	4	US-10-196-927-5
18	119.6	5.0	2765	4	US-09-799-451-50
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22	106.8	4.5	906	3	US-09-221-527-3
23	106.8	4.5	906	3	US-09-221-236-3
24	106.8	4.5	906	3	US-09-221-416-3
25	106.8	4.5	906	3	US-09-221-245-3
26	106.8	4.5	906	3	US-09-163-115-3
27	106.8	4.5	906	3	US-09-221-528-3

28	106.8	4.5	906	3	US-09-593-553-3	Sequence 3, Appli
29	106.8	4.5	906	3	US-09-221-237-3	Sequence 3, Appli
30	106.8	4.5	906	4	US-09-757-982-3	Sequence 3, Appli
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34	106.8	4.5	4137	3	US-09-221-236-1	Sequence 1, Appli
35	106.8	4.5	4137	3	US-09-221-416-1	Sequence 1, Appli
36	106.8	4.5	4137	3	US-09-221-245-1	Sequence 1, Appli
37	106.8	4.5	4137	3	US-09-163-115-1	Sequence 1, Appli
38	106.8	4.5	4137	3	US-09-221-528-1	Sequence 1, Appli
39	106.8	4.5	4137	3	US-09-593-553-1	Sequence 1, Appli
40	106.8	4.5	4137	3	US-09-221-237-1	Sequence 1, Appli
41	106.8	4.5	4137	4	US-09-757-982-1	Sequence 1, Appli
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43	100	4.2	1060	4	US-10-355-975A-2	Sequence 2, Appli
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45	86.2	3.6	4880	3	US-09-031-563-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-873-404-1

; Sequence 1, Application US/09873404

; Patent No. 6500656

; GENERAL INFORMATION:

; APPLICANT: WEBSTER, Marion et al

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THREEOF

; FILE REFERENCE: CL001212-CIP

; CURRENT APPLICATION NUMBER: US/09/873,404

; CURRENT FILING DATE: 2001-06-05

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 2370

; TYPE: DNA

; ORGANISM: Human

; US-09-873-404-1

Query Match 100.0%; Score 2370; DB 4; Length 2370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	121	TTGAAAAGATGCCCATACAGAAAAGAGCTTCAAAAGAAAGTGAATCTTCTTGAAA	180
Qy	181	AGATGAACATCCCAACATTTAGTCCCTTCTCAATTCATTCAGAGAATGGCAGGCTGT	240
Db	181	AGATGAACATCCCAACATTTAGTCCCTTCTCAATTCATTCAGAGAATGGCAGGCTGT	240
Qy	241	TTATTGTAATGGAAATTTGTGATGGAGGGATCTCATGAAAAGGATCAATAGACAACGGG	300
Db	241	TTATTGTAATGGAAATTTGTGATGGAGGGATCTCATGAAAAGGATCAATAGACAACGGG	300
Qy	301	GTGTGTTATTAGTGAAGATCAGATCCTCGGTGGTTGTACAGATTTCTTAGACTAA	360
Db	301	GTGTGTTATTAGTGAAGATCAGATCCTCGGTGGTTGTACAGATTTCTTAGACTAA	360
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481	Qy	CCATGGAA	CTGCTCGAACTTGTATTTGGAACACCTTTACTACTCTCTCCAGAGATCTGTCT	540
481	Db	CCATFGAA	CTGCTCGAACTTGTATTTGGAACACCTTTACTACTCTCTCCAGAGATCTGTCT	540
541	Qy	AGAATAAA	CCCTACAAACAATAAAACGGATATTGGTCTCTCTGGGTGTCTTATATGAGC	600
541	Db	AGAATAAA	CCCTACAAACAATAAAACGGATATTGGTCTCTCTGGGTGTCTTATATGAGC	600
601	Qy	TCTGCACA	CTTTAAACATCTCTTTTGAGGGTAAACAATTCACAGCAGCTGGTTCTGAAGATT	660
601	Db	TCTGCACAT	TTAAACATCTCTTTTGAGGGTAAACAATTCACAGCAGCTGGTTCTGAAGATT	660
661	Qy	GTCAAGCACA	TTTTGCCCAATATCTCCGGGGTTTTCTCGGGAGTCTCGTGAGCTCCATTTCCTTGATAT	720
661	Db	GTCAAGCACA	TTTTGCCCAATATCTCCGGGGTTTTCTCGGGAGTCTCGTGAGCTCCATTTCCTTGATAT	720
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721	Db	CTCAGCTCT	TTTCAAGTATCTCTCTCGAGACGAGCACCATCCATAAATTCATTTTGAAGAGGC	780
781	Qy	CCTTTTTAGA	GATCTTTATCCCAAAATATTGACTCTTGAGGTCAATTCAGGAGAATTC	840
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841	Qy	GTCAATGCT	TTATATGACAGACGAGGCGCAGCTTCTCGACATGCTGGGAAGTGTCTCC	900
841	Db	GTCAATGCT	TTATATGACAGACGAGGCGCAGCTTCTCGACATGCTGGGAAGTGTCTCC	900
901	Qy	AGAAGTGTAA	ATAAATAAGTAGAGATTCCGGGAAAGTGCCCAACCAAGATCAAGAGTAT	960
901	Db	AGAAGTGTAA	ATAAATAAGTAGAGATTCCGGGAAAGTGCCCAACCAAGATCAAGAGTAT	960
961	Qy	CTGTGCCAA	TTTAAAGGAATGCTATATTGCATAGAAATGAATGAGACACCCAGCTCGAG	1020
961	Db	CTGTGCCAA	TTTAAAGGAATGCTATATTGCATAGAAATGAATGAGACACCCAGCTCGAG	1020
1021	Qy	CCCAAGGCG	CAGATCTATAAATAATGATAGAAAGCCCAAAATTTGCTGTCTGTGGAC	1080
1021	Db	CCCAAGGCG	CAGATCTATAAATAATGATAGAAAGCCCAAAATTTGCTGTCTGTGGAC	1080
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1141	Db	ATCACCTAT	TTCTCAAGAAATACTCGAGTTGAGGATTAACGTCAGGAAACAGGCGATG	1200
1201	Qy	GTCCATCCC	CAAGTCAATGCGCTGCTGAGTACCTTCAGAGAAATTTGAGCTCAACAAT	1260
1201	Db	GTCCATCCC	CAAGTCAATGCGCTGCTGAGTACCTTCAGAGAAATTTGAGCTCAACAAT	1260
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1261	Db	ATAAGTTGA	AGTGGAGAACAAATTTGGTCTTCCTCCATCTTCTGCCAGGCCAAATTACA	1320
1321	Qy	ACCAGAGACA	AGAGCTTAAGAGTAATTTGAGAGAGAGCTTAGATTCCAGGAGCTGCCATTTA	1380
1321	Db	ACCAGAGACA	AGAGCTTAAGAGTAATTTGAGAGAGAGCTTAGATTCCAGGAGCTGCCATTTA	1380
1381	Qy	GGAAAAAC	GAAATGAAAGAACAGGAATTTTGAAGCAGATTAGAGGAAATACGCCAACGT	1440
1381	Db	GGAAAAAC	GAAATGAAAGAACAGGAATTTTGAAGCAGATTAGAGGAAATACGCCAACGT	1440
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RESULTS. T. 2

RESULT 2
US-10-243-735-1

03 10 23 733 1
; Sequence 1, Application US/10243735

; Patent No. 6706510

GENERAL INFORMATION:

APPLICANT: WEBSTER, Marion et al

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL001212DIV

; CURRENT APPLICATION NUMBER: US/10/243,735

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; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2370
; TYPE: DNA
; ORGANISM: Human
US-10-243-735-1

Query Match
Best Local Similarity 100.0%; Score 2370; DB 4; Length 2370;
Matches 2370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTGGAGACCATGGATAGTACGATGCTGATTAAGCCATCGGCAAGTGCCTTCGGGA 60
DB 1 CATTGGAGACCATGGATAGTACGATGCTGATTAAGCCATCGGCAAGTGCCTTCGGGA 60
QY 61 AAGCATACCTAGTAAAGGGAATCAGATAGCAAGCACTGTCTATAAAGAGATCAATT 120
DB 61 AAGCATACCTAGTAAAGGGAATCAGATAGCAAGCACTGTCTATAAAGAGATCAATT 120
QY 121 TTGAAAAGATGCCATACAAAGAAAAGAGCTTCAAAGAAAGATGATTTCTTGGAAA 180
DB 121 TTGAAAAGATGCCATACAAAGAAAAGAGCTTCAAAGAAAGATGATTTCTTGGAAA 180
QY 181 AGATGAAACATCCCAACATTTAGCTTCTTCAATTCATTTCAAGAGAAATGCGAGCTGT 240
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QY 241 TTATGTGAATGAATATTGTGATGGAGGGATCTCATGAAAAGGATCAATAGACAACGG 300
DB 241 TTATGTGAATGAATATTGTGATGGAGGGATCTCATGAAAAGGATCAATAGACAACGG 300
QY 301 GTGTGTTATTAGTGAAGATCAGATCCCTCGTGTGTTGTACAGATTTCTCTAGACTAA 360
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DB 361 AACATATTCAATGACAGGAGATATTACACAGGACATAAAGCTCAGAAACATTTTCTTA 420
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DB 421 GCAAGAACGGAATGTGGCAAGCTTGGGACTTTGGTATAGCAAGATCTCGTAAATTT 480
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DB 601 TCTGCACACTTAAACATCTTTTGGGGTAAACATTTACAGCAGCTGTTCTGAGATTT 660
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DB 1861 TTGAGGATCTCTTTGTGCCAACGACTGCTCACTGAAGGACTGGAGTGAAGGAAATGG 1920
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QY 1981 GCCAAAGGAGAGAGACAGGTCATGGGGAGGCAAGGAATTTGGCAGCATCAACTGGGAAGA 2040
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; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunding
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_PL_genes Version 1.0
; SEQ ID NO 245
; LENGTH: 5532
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (534)...(4262)
; US-09-620-312D-245

Query Match 15.6%; Score 369.4; DB 4; Length 5532;
Best Local Similarity 66.0%; Pred. No. 1.5e-97;
Matches 551; Conservative 0; Mismatches 281; Indels 3; Gaps 1;

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DB 531 ATCATGGGAAGTATGTTAGACTACAGAAGATGGAGAAGGTTCATTGGGAAGCCATT 590
QY 69 TTAGCTAAAGGGAAATCAGATAGCAAGCACTGTGTCTATAAAAGAGATCAATTTTGAAG 128
DB 591 CTGTGTTAATCTACAGAAGTGGCAGACAGTATGTTATCAAGAAATTAACATCTCAGA 650
QY 129 ATGCCCATACAGAAAAGAGCTTCAAGAAAGAGTCAATCTCTGGAAAAGATGAAA 188
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QY 429 GGAATGGTGGAAAGCTTCGGGACTTTGGTATAGCMAGAGTCTCGAATATTCATGGAA 488
DB 951 GGAACAGT---ACAACCTCGAGATTTTGGAAATTTGCTAGAGTCTTAAATAGTACTGTAGAG 1007
QY 489 CTTCGCTCGAACTGTATTGGAAACACCTTACTACCTGTCGCCAGAGATCTGTCAAGATAAA 548
DB 1008 CTGGCTCGAACTGTGATAGGGACCCCATACTACTGTCTACCTGAAATCTGTGAAAACAAA 1067
QY 549 CCTTACAAACAATAAAGCGATATTTGGTCTCTTGGCTGTGTCTTATAGAGCTCTGCA 608
DB 1068 CCTTACAATAAATAAAGTGACATTTGGGCTCTGGGCTGTGTCTTATGAGCTGTGTACA 1127
QY 609 CTTAATACCTTTTCAGGGTAACTATTACAGCAGCTGTTCTGAAGATTTGTCAAGCA 668
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Db 1128 CTTAAACATGCTTTTGAAGCTGGCAGTATGAAAAAACCTGGTACTGAAGATAATATCTGGA 1187
QY 669 CATTTTGCCTCAATATCTCGGGGTTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTC 728
Db 1188 TCCTTTCCACTGTGTCTTTTGCATTATCTCTATGATCTCCGAGTTTGGTGTCTCAGTTA 1247
QY 729 TTTCAAGTATCTCTCGAGACCGACCATCCATATAATTTCCATTTTGAAGAGCCCTTTTAA 788
Db 1248 TTTAAAGAAATCTTAGGATAGACCATCAGTCACTCCATATTGGAGAAAGGTTTATA 1307
QY 789 GAGAATCTTATTTCCAAATATTTGACCTCCGAGGTCAATTCAGGAAGAAATTCAGTC 843
Db 1308 GCCAAACGCATTGAAAGTTTCTCTCTCTCAGCTTATTGCAAGAAATTTTGTG 1362

RESULT 5
US-09-166-350-29
; Sequence 29, Application US/09166350A
; Patent No. 6440863
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Chen, Yao
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Old, Lloyd
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alex
; TITLE OF INVENTION: Renal Cancer Associated Antigens and
; FILE REFERENCE: L0461/7051
; CURRENT APPLICATION NUMBER: US/09/166,350A
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: US 09/166,350
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 4263
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-166-350-29

Query Match 15.0%; Score 355.8; DB 4; Length 4263;
Best Local Similarity 64.8%; Pred. No. 1.3e-93;
Matches 544; Conservative 0; Mismatches 292; Indels 3; Gaps 1;

QY 5 GGAGACCATGGATGAAGTACGATGTGATTAGGCCATCGGCCAGGTGCTTCGGGAAGC 64
DB 569 GGGAAACCATGGAGAAGTATGTGAGACTGCAGAAAGATTGGAGAAGTTTCATTTGGAAAAGC 628
QY 65 ATACTTAGCTAAAGGGAAATCAGATAGCAAGCACTGTGTCTATAAAAGAGATCAATTTTGA 124
DB 629 TGTTCCTTGTAAATCGACAGAGGATGCAGACATTATGTCTCAAGGAATTAACATCTC 688
QY 125 AAAGATGCCCATACAGAAAAGAGCTTCAAGAAAGAGAGTGTATTTCTCTGGAAGAAAT 184
DB 689 AAGAATCTCTGATAAAGAAAGGCAAGAAATCAAGGAGAGAAGTTGCTGTATTGGCAACAT 748
QY 185 GAAACATCCCAACATTTGAGCTTCTTCAATTTCAAGAGAAGTGGCAGGCTGTTTAT 244
DB 749 GAACATCCCAATATTTCTCAATATAAAGAAATCATTTTGAAGAAATGCTCTCTCTACAT 808
QY 245 TGTAATGGAATATTTGATGGAGGGATCTCATGAAAGAGATCAATAGACAACGGGCTGT 304
DB 809 AGTAATGGATTACTGTCAAGGAGGTGATTTGTTTAAACGAATAAATGCTCAGAAAGCGC 868
QY 305 GTTATTTAGTGAAGATCAGATCTCGGTTGGTTGTACAGATTTCTTAGACTATAACA 364
DB 869 TCTGTTTCAAGAGACACAGATTTTGGACTGGTTGTGAGATATGTTTGGCTCTGAAGCA 928
QY 365 TATTTCATCAGAGGAAGATATTACACAGGGACATATAAAGCTCAGAACATTTTCTTAGCAA 424
DB 929 TGTACATGATAGAAAATTTCTTCAAGGAGACATAAAGTACAGAACATATTCTTCAACAA 988
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QY 425 GAACGGAATGGTGGCAAGCTTTGGGAGATTTGGTATAGCAAGATCTCTGAATATATTCAT 484
Db 989 AGATGGGACAGTG---CAGCTTGGAGATTTTGGAAATTTCTCGAGTTCTTAATAGTACTGT 1045
QY 485 GGAACCTTCTCGAATCTGTATTGGAACACCTTACTACTGCTGCCAGAGATCTGTGAGAA 544
Db 1046 AGAGCTGGCTGAACTTGCAATAGGACCTCCATATCTATTGTCACCTGAAATCTGTGAAA 1105
QY 545 TAAACCCCTACACAATAAAACGGATATTGGTCTCTTTGGCTGTCTTATATAGCTCTG 604
Db 1106 CAAGCCTTATAACAATAAAAGTGACATTTGGGCTTTGGGCTGTCTCTTTATGAGTTGTG 1165
QY 605 CACACTTAAACATCTTTTGGAGGTACAACTTACAGCAGCTGGTTCTGAGATTTGTCA 664
Db 1166 TACACTTAAACATGATTTGAAGCTTGGAAACATGAAAACCTGTACTGGAAGATAATCTC 1225
QY 665 AGCAGATTTTCCCAATATCTCCGGGTTTTCTCTGAGCTCCATTTCTCTTGATATCTCA 724
Db 1226 CGGATCCTTCTCCAGGTCTCCACATTTACTCTCTATGATCTCCGAGCTTGTCTCTCA 1285
QY 725 GCTCTTCAAGTATCTCTCGAGACCGACATCCATTAATTCATTTTGGAAAGGCCCTT 784
Db 1286 GTTATTTAAAGAAATCTTAGGGATAGACCATCAGTCAATCCATATTGGAGAAAGGTTT 1345
QY 785 TTTAGAGATCTTATTTCCAAATATTGACTCTCTGAGTCAATTCAGGAAGATTCAGTC 843
Db 1346 TATAGCTAAACGAATCGAAGATTTCTCTCCCTCAGCTTATTGCAGAGATTTTGTG 1404

RESULT 6

US-09-173-581-15
; Sequence 15, Application US/09173581A
; Patent No. 6013455

GENERAL INFORMATION:

; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Gorgone, Gina
; APPLICANT: Azimzai, Yalda
; APPLICANT: Lu, Aina
; TITLE OF INVENTION: Protein Kinase Homologs
; FILE REFERENCE: PF-0614 US
; CURRENT APPLICATION NUMBER: US/09/173,581A
; EARLIER FILING DATE: 1998-10-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PERL Program
; SEQ ID NO 15
; LENGTH: 1846
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1567782

US-09-173-581-15

Query Match 10.1%; Score 238.4; DB 3; Length 1846;
Best Local Similarity 67.5%; Pred. No. 2.1e-59;
Matches 351; Conservative 0; Mismatches 166; Indels 3; Gaps 1;

QY 324 ATCCCTCGTGGTTGTACAGATTTCTTAGGACTTAAACATATTCTATGACAGGAAGATA 383
Db 370 ATTTGGACTGGTTGTACAGATATGTTGGCCCTGAAACATGTACATGATAGAAAATT 429
QY 384 TTACACAGGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGATGGTGGCAAG 443
Db 430 CTTCATCGAGACATTAATCTCAGACATATTTTAACTAAGATGGAACAGT---ACAA 486
QY 444 CTTGGGACTTTGGTATAGCAAGTCTCGAATTAATTCATGGAACCTTGTCTGCAACTTGT 503
Db 487 CTTGGAGATTTTGGAAATTTGCTAGAGTTCTTAATAGTACTGTAGAGCTGGCTCGAACTTGC 546

QY 504 ATTGGAACACCTTACTACTGTCCTCCAGAGATCTGTCTAGAAATAAACCTCAACAATAAA 563
Db 547 ATAGGGACCCCACTACTACTTGTCACTGAAATCTGTGAAAAACAACCTTACAATAATAA 606
QY 564 ACGGATATTTGGTCTCTTGGCTGTCTTATATAGCTCTGCACACTTAAACATCTCTTT 623
Db 607 AGTGACATTTGGGCTCTGGGTTGTCTTATGAGCTGTGTACACTTAAACATGCTTTT 666
QY 624 GAGGTAACAACTTACAGCAGCTGGTTCTGAAGATTTTCTCAAGCACATTTTGGCCCCAATA 683
Db 667 GAAGCTGGCAGTATGAAAAACCTGTACTGAAGATAATATCTGGATCTTTTCCACCTGTG 726
QY 684 TCTCCGGGTTTTCTCGTGCAGCTCCATTTCTTGATATCTCAGCTCTTCAAGTATCTCT 743
Db 727 TCTTTGCAATTTCTCTATGATCTCCGAGTTTGGTGTCTCAGTTATTTTAAAGAAATCTT 786
QY 744 CGAGACCCGACCATCCATTAATTTCCATTTTGAAGGCCCTTTTATAGAAATCTTTATCCC 803
Db 787 AGGGATAGACCATCAGTCACTCCATATTGGAGAAAGGTTTTATAGCCAAACGCATTGAA 846
QY 804 AAATATTTGACTCTCTGAGTCAATTCAGGAAGATTCAGTC 843
Db 847 AAGTTTCTCTCTCTCAGCTTATTGCAGAGAAATTTTGTG 886

RESULT 7

US-09-420-915-15
; Sequence 15, Application US/09420915
; Patent No. 6264947

GENERAL INFORMATION:

; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Gorgone, Gina
; APPLICANT: Azimzai, Yalda
; APPLICANT: Lu, Aina
; TITLE OF INVENTION: Protein Kinase Homologs
; FILE REFERENCE: PF-0614 US
; CURRENT APPLICATION NUMBER: US/09/420,915
; EARLIER FILING DATE: 1999-10-20
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/173,581
; EARLIER FILING DATE: 1998-10-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PERL Program
; SEQ ID NO 15
; LENGTH: 1846
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1567782

US-09-420-915-15

Query Match 10.1%; Score 238.4; DB 3; Length 1846;
Best Local Similarity 67.5%; Pred. No. 2.1e-59;
Matches 351; Conservative 0; Mismatches 166; Indels 3; Gaps 1;

QY 324 ATCCCTCGTGGTTGTACAGATTTCTTAGGACTTAAACATATTCTATGACAGGAAGATA 383
Db 370 ATTTGGACTGGTTGTACAGATATGTTGGCCCTGAAACATGTACATGATAGAAAATT 429
QY 384 TTACACAGGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGATGGTGGCAAG 443
Db 430 CTTCATCGAGACATTAATCTCAGAACATATTTTAACTAAGATGGAACAGT---ACAA 486
QY 444 CTTGGGACTTTGGTATAGCAAGTCTCGAATTAATTCATGGAACCTTGTCTGCAACTTGT 503
Db 487 CTTGGAGATTTTGGAAATTTGCTAGAGTTCTTAATAGTACTGTAGAGCTGGCTCGAACTTGC 546
QY 504 ATTGGAACACCTTACTACTCTCTCCAGAGATCTGTCTAGAAATAAACCTCAACAATAAA 563

Db 547 ATAGGACCCCATACTACTGTGACCTGAATCTGTGAAAAACAACCTTACATAATAA 606
Qy 564 ACGATATTTGGTCTCTGGCTGTGCTTATATGAGCTCTGCACATTAACAATCTTTT 623
Db 607 AGTGACATTTGGGCTCTGGGCTGTGCTTATGAGCTGTGTACACTTAAACATGCTTT 666
Qy 624 GAGGTAACAACCTTACAGCAGCTGGTCTCGAAGATTGTCAAGCACAATTTGCCCCAATA 683
Db 667 GAAGCTGGCAGTATGAATAACCTGGTACTGAAGATAATATCTGATCTTTTCCACCTGTG 726
Qy 684 TCTCCGGGTTTCTCTGCTGAGCTCCATTCCTTCTGATATCTCAGCTCTTTCAAGTATCTCCT 743
Db 727 TCTTGCATTATCTCTATGATCTCCGAGTTTGGTGTCTCAGTTATTTAAAGAAATCCT 786
Qy 744 CGAGACCGACATCCATAAATTCATTTTGAAGGCCCTTTTAGAGATCTTATCC 803
Db 787 AGGATAGACCATCAGTCAACTCCATTCATTCGGAAGAGTTTATAGCCAAACGATTGAA 846
Qy 804 AATATTGACTCTCTGAGGTCATTTCAGGAAGAATTCAGTC 843
Db 847 AAGTTCTCTCTCTCAGCTATTTCGAGAAGAATTTTGTIC 886

RESULT 8
US-09-873-404-3
; Sequence 3, Application US/09873404
; Patent No. 650656
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001212-CIP
; CURRENT APPLICATION NUMBER: US/09/873,404
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 63588
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(63588)
; OTHER INFORMATION: n = A,T,C or G
US-09-873-404-3

Query Match 8.7%; Score 205.2; DB 4; Length 63588;
Best Local Similarity 96.3%; Pred. No. 1.2e-48;
Matches 210; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 617 TCTTTTGGGGTAAACAATTACAGCAGCTGGTCTGAAAGATTGTCAAGCACAATTTTGC 676
Db 27430 TCAGTTTGGGGTAAACAATTACAGCAGCTGGTCTGAAAGATTGTCAAGCACAATTTGC 27489
Qy 677 CCCAATATCTCCGGGTTTCTCGTGAAGTCCATTCCTTGATATCTCAGCTCTTTCAAGT 736
Db 27490 CCCAATATCTCCGGGTTTCTCGTGAAGTCCATTCCTTGATATCTCAGCTCTTTCAAGT 27549
Qy 737 ATCTCTCGAGACCGACCATCCATAAATTCATTTGAAAGGCCCTTTTAGAGAATCT 796
Db 27550 ATCTCTCGAGACCGACCATCCATAAATTCATTTGAAAGGCCCTTTTAGAGAATCT 27609
Qy 797 TATTCCTCGAGACCGACCATCCATAAATTCATTTGAAAGGCCCTTTTAGAGAATCT 834
Db 27610 TATTCCTCGAGACCGACCATCCATAAATTCATTTGAAAGGCCCTTTTAGAGAATCT 27647

; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001212-DIV
; CURRENT APPLICATION NUMBER: US/10/243,735
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 63588
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(63588)
; OTHER INFORMATION: n = A,T,C or G
US-10-243-735-3

Query Match 8.7%; Score 205.2; DB 4; Length 63588;
Best Local Similarity 96.3%; Pred. No. 1.2e-48;
Matches 210; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 617 TCTTTTGGGGTAAACAATTACAGCAGCTGGTCTGAAAGATTGTCAAGCACAATTTTGC 676
Db 27430 TCAGTTTGGGGTAAACAATTACAGCAGCTGGTCTGAAAGATTGTCAAGCACAATTTGC 27489
Qy 677 CCCAATATCTCCGGGTTTCTCGTGAAGTCCATTCCTTGATATCTCAGCTCTTTCAAGT 736
Db 27490 CCCAATATCTCCGGGTTTCTCGTGAAGTCCATTCCTTGATATCTCAGCTCTTTCAAGT 27549
Qy 737 ATCTCTCGAGACCGACCATCCATAAATTCATTTGAAAGGCCCTTTTAGAGAATCT 796
Db 27550 ATCTCTCGAGACCGACCATCCATAAATTCATTTGAAAGGCCCTTTTAGAGAATCT 27609
Qy 797 TATTCCTCGAGACCGACCATCCATAAATTCATTTGAAAGGCCCTTTTAGAGAATCT 834
Db 27610 TATTCCTCGAGACCGACCATCCATAAATTCATTTGAAAGGCCCTTTTAGAGAATCT 27647

RESULT 10
US-09-992-481-1
; Sequence 1, Application US/09992481
; Patent No. 6593125
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; APPLICANT: Mathur, Brian
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6593125el Human Kinases and Polynucleotides
; FILE REFERENCE: LEX-0266-USA
; CURRENT APPLICATION NUMBER: US/09/992,481
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/252,011
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2079
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-992-481-1

Query Match 7.2%; Score 170.2; DB 4; Length 2079;
Best Local Similarity 52.1%; Pred. No. 2.4e-39;
Matches 404; Conservative 0; Mismatches 368; Indels 3; Gaps 1;

Qy 12 ATGATAGTACGATGTGATTAAGCCATCGGCAAGTCCCTTCGGGAAGCATCTTA 71
Db 1 ATGGAAGAAGTACGAGCGGATCCGAGTGTGCGGAGAGGTCCCTTCGGGATTTGCACTG 60
Qy 72 GCTAAGGGAAATCAGATAGCAAGCACTGTGTCTATAAAGAGATCAATTTTGAAGAATG 131

Db 61 TGCTGGAAAGGCTGACCAAGAGCTGGTGTATCATCAAGCAGATTCCAGTGGACAGATG 120
Qy 132 CCCATACAAAGAAAGAGCTTCAAAAGAAAGAGTATCTTCTGGAAAAGATGAACAT 191
Db 121 ACCAAGGAAGAGCGGACGAGCCAGAAATGAGTCCAGAGTCTCTCAAGCTGCTCAACAC 180
Qy 192 CCCACATGTAGCTCTCTCAATTCATTCATCAAGAGATGCGAGCGTGTATTTGTAATG 251
Db 181 CCCATGTCAATGAGTACTAGAGACTTCTTGGAGACAAAGCCCTATGATCGGCATG 240
Qy 252 GAATATTGTGAGGAGGATCTCATGAAAGAGTCAATAGACAAACGGGTGTGTTATTT 311
Db 241 GAATATGCACAGCGGACCTCTGGCTGAGTTCATCCAAAAGCGCTGTAATCCCTGCTG 300
Qy 312 AGTGAAGATCAGATCCTCGGTGGTGTGTGTACAGATTTCTTAGACTAAACATATTCAT 371
Db 301 GAGGAGGAGACCATCTCTGCACTTCTTGTGAGATCCTGCTTGCACTGCAATGTCAC 360
Qy 372 GACAGGAAGATATTACAGAGGACATAAAGCTCAGAACATTTTCTTAGCAAGAACGA 431
Db 361 ACCACCTCATCTCCACCGAGACTCAAGACCCAGAACATCTCTGCTTGACAAACACCGC 420
Qy 432 ATGGTGGAAAGCTTGGGAGCTTTGGTATAGCAAGAGTCTCTGAATATTCATGTAATTC 491
Db 421 ATGGTCTGCAAGATCGGTGATTTCCGGCATCTCCAGATCCT---TAGCAGGAGAGCAAG 477
Qy 492 GCTCAACTGTGATTGGAACACCTTACTACTCTGCCCCAGAGATCTCTGCAAGATAAACCC 551
Db 478 GCCTACAGGTGGTGGTACCCCATGCTATATCTCCCTGAGCTGTGTGAGGGCAAGCCC 537
Qy 552 TACAAACAATAAAGGATATTGTTGTTCTTGGCTGTGTCTTATATGAGCTCTGCACACTT 611
Db 538 TACAACCAAGAGAGTACATCTGGGCCCTGGGCTGTCTCTACGAGCTGGCCAGCCTC 597
Qy 612 AAACATCTTTTGGAGTAAACAATTACAGCAGCTGGTCTGGAAGATTTGTCAAGCACAT 671
Db 598 AAGAGGGCTTCGAGGCTGCGAACTTGCAGCACTGGTGTCTGAAGATCATGAGTGGCACC 657
Qy 672 TTTGCCCAATATCTCCGGGGTTTTCTCGTGGCTTCCATTCCTTTGATATCTCAGCTCTTT 731
Db 658 TTTGCACTATCTCTGACCGGTACAGCCCTGAGCTTGGCCAGCTGGTCTGAGTCTACTC 717
Qy 732 CAGATATCTCTGAGACGACCATCCATAATTCATTTTGAAGAGCCCTTTT 786
Db 718 AGCCTGGAGCTGCCAGCGGCCACCACCTACGCCACATCATGGCACAGCCCTCT 772

RESULT 11

US-08-870-529-1
; Sequence 1, Application US/08870529
; Patent No. 6080557
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Virca, G. Duke
; APPLICANT: Bird, Timothy A.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: IL-1/TNF-(-ACTIVATED KINASE (ITAK),
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESS: SEED and BERRY LLP
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/870,529
; FILING DATE: 06-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2940 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2937
; US-08-870-529-1

Query Match 7.0%; Score 166.8; DB 3; Length 2940;
Best Local Similarity 54.8%; Pred. No. 3e-38;
Matches 352; Conservative 0; Mismatches 287; Indels 3; Gaps 1;

Qy 36 GCATCGGGCAAGTGCCTTCGGGAAGCATACATTAGCTAAAGGGAATCAGATAGCAAG 95
Db 169 GTCTGGGCGCGGCGCCTTCGGGAAGCCACGCTGTACCCGCCGCCAGGATGACTCA 228
Qy 96 CACTGTGTCTATAAAGAGATCAATTTTGAAGAAGATGCCCATACAAGAAAAAGAGTTCA 155
Db 229 CTGTTGTGTGAAGAGAGTGCATTTTGACCGGCTGTCTGAGAGGAACGCTCGTGATGCC 288
Qy 156 AAGAAGAGAGTGAATTTCTGGAAGAGATGAACATCCCAACATTTGAGCTTCTTCAAT 215
Db 289 TTGAATAGATAGTATTATTCTGGCACTGCTGAGCAACGACATTAATTCCTACTACAT 348
Qy 216 TCATTTCAAGAGAGTGGCAGGCTGTTTATTGTAATGAATATTGTGATGGAGGGGATCTC 275
Db 349 CACTTCATGAGCAATACACGCTGCTGATGAGCTGGATATTGTAATGGAGGAACCTG 408
Qy 276 ATGAAAAGAGATCAATAGACAACCGGGTGTGTTATTAGTGAAGATCAGATCCTCGGTTGG 335
Db 409 TATGACAAAATCCTTCGTGAGAAAGCAAGTTGTTTGAGGAAGAGATGCTGTGTGTAC 468
Qy 336 TTTGTACAGATTTCTTAGGACTAAACATATTCATGACAGGAAGATATTACACAGGAC 395
Db 469 CTATTCAGATTTCTTACGAGTGTGCTGATCCATTAAGCTGGATCTCTTCATAGAT 528
Qy 396 ATAAAGAGCTCAGAACATTTTCTTAGCAAGAACCGAATGGTGGCAAGCTTGGGACTTT 455
Db 529 ATAAAGACATTAATATTTTCTGACCAAG---GCAACCTGATAAACTTGGAGATTAT 585
Qy 456 GGTATAGGAAGAGTCTGATTAATTCATGGAATTCCTGGAATTTGTTGGAACACT 515
Db 586 GGCCTAGCAAGAAACTTAATTTCTGAGTATTCATGGCTGAGACGCTTGTGGAAACCCA 645
Qy 516 TACTACTGTCCCGCAGAGATCTGTGAGATAAACCTACAAATATAAAGCGATTTGG 575
Db 646 TATTACATGTTCCAGAGCTCTGTCAAGGAGTAAAGTACAATTTCAAGTCTGATATCTGG 705
Qy 576 TCTTTGGTGTGTTTATATGAGCTCTGCACACTTAACATCTCTTTGAGGTTAACAC 635
Db 706 GCAGTTGGTGTGCTATTTTGAAGTCTTACCTTAAAGAGAGACGTTGATCTCTAAAC 765
Qy 636 TTACAGCAGCTGTTCTGAGGATTTGTCAAGCACATTTTGCC 677
Db 766 CCATTAACCTGTGTGTGAAGATCTGTGCAAGGAATTCGGGCC 807

RESULT 12
US-09-544-794-1
; Sequence 1, Application US/09544794

Patent No. 6541232
GENERAL INFORMATION:
APPLICANT: Sims, John E.
APPLICANT: Virca, G. Duke
APPLICANT: Bird, Timothy A.
APPLICANT: Anderson, Dirk M.
FILE REFERENCE: 2005-B
CURRENT FILING DATE: 2000-04-07
PRIORITY APPLICATION NUMBER: US/09/544,794
PRIORITY FILING DATE: 1997-06-06
PRIORITY APPLICATION NUMBER: 60/059,979
PRIORITY FILING DATE: 1996-06-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2940
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2940)
US-09-544-794-1

Query Match 7.0%; Score 166.8; DB 4; Length 2940;
Best Local Similarity 54.8%; Pred. No. 3e-38;
Matches 352; Conservative 0; Mismatches 287; Indels 3; Gaps 1;

QY	36	GCATCGGCGCAGGTCCTTCGGGAAGCATACTAGCTAAAGGAAATCAGATAGCAAG	95
Db	169	GTCTGGCGCGCGCCCTTCGGGAAGCCACGCTGTACCGCGCCAGGAGACTCA	228
QY	96	CACCTGTGTATAAAGAGATCAATTTTGAAGAAGTCCCATACAGAAAAGAACTTCA	155
Db	229	CTGGTTGTGTGAAGGAAGTCGATTGTACCGCGCTGTCTGAGAAGAACGTCGTATGCC	288
QY	156	AGAAGAAGTGAATCTTCGGAAGAAGTGAACATCCCAATTTGAGCTTCTTCAAT	215
Db	289	TTGAATGAGATAGTATTCTGCACTGTCTGACAGCAGCAACATTTTGCCTACTACAT	348
QY	216	TCATTTCAAGAGAATGGCAGGCTGTTTATTGTAATGGAATATTGTATGGAGGGATCTC	275
Db	349	CACCTCATGACAATACCACGCTGTGATTGAGCTGGATATTGTAATGGAGGAACTG	408
QY	276	ATGAAAAGGATCAATAGACAACGGGGTGTATTATTAGTAGAGATCAGATCCTCGTTGG	335
Db	409	TATGACAAAATCCTTCGTGAGAGGACAAAGTGTGTTGAGGAAGAGATGCTGTGTGTAC	468
QY	336	TTTGTACAGATTTCTAGGACTTAAACATATTTCAATGACAGAGATATTACAGGGAC	395
Db	469	CTATTTCAAGATTTCTAGGACTTAAACATATTTCAATGACAGAGATATTACAGGGAC	528
QY	396	ATPAAAGCTCAGAACATTTTCTAGCAAGAACGGAATGGTGGCAAGCTTTGGGACATT	455
Db	529	ATPAAAGACATTAATATTTTCTGACCAAG--GCAAACTGATAAACTTTGGAGATTAT	585
QY	456	GGTATGCAAGAGTCTGATTAATTCATGGAATGCTGCACTGCTGCACTGCTGCACTG	515
Db	586	GGCCTAGCAAGAACTTAATTTCTGAGTATTCATGCTGAGAGCTTTGTTGGGACCCCA	645
QY	516	TACTACCTGTCCCGCAGAGATCTGTGAGAAATTAACCTTACAAATATAAGCGATATTGG	575
Db	646	TATTACATGCTCTCCAGAGCTCTGTGACAGGAGTAAAGTACATTTCAAGTCTGATCTGG	705
QY	576	TCTCTTGGTGTGCTTATAGAGCTCTGACACTTAAACATTCCTTTTGGAGGGTAAACAC	635
Db	706	GCAGTTGGCTGGCTCAATTTTGAATGCTTACCTTAAAGAGAGAGCTTTGATGCTACAAAC	765
QY	636	TTACAGCAGCTGGTCTCAAGATTTGTCAAGACATTTTGGC	677
Db	766	CCACTTAACCTGTGTGTGAGATCTGTGCAAGGAATTCGGGCC	807

RESULT 13
US-08-870-529-8
Sequence 8, Application US/08870529
Patent No. 6080557
GENERAL INFORMATION:
APPLICANT: Sims, John E.
APPLICANT: Virca, G. Duke
APPLICANT: Bird, Timothy A.
APPLICANT: Anderson, Dirk M.
TITLE OF INVENTION: IL-1/TNF- α -ACTIVATED KINASE (ITAK),
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,529
FILING DATE: 06-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3264 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-870-529-8

Query Match 7.0%; Score 166.8; DB 3; Length 3264;
Best Local Similarity 54.8%; Pred. No. 3.3e-38;
Matches 352; Conservative 0; Mismatches 287; Indels 3; Gaps 1;

QY	36	GCATCGGCGCAGGTCCTTCGGGAAGCATACTAGCTAAAGGAAATCAGATAGCAAG	95
Db	288	GTCTGGCGCGCGCCCTTCGGGAAGCCACGCTGTACCGCGCCAGGAGTACTCA	347
QY	96	CACCTGTGTATAAAGAGATCAATTTTGAAGAAGTCCCATACAGAAAAGAACTTCA	155
Db	348	CTGGTTGTGTGGAAGGAGTCTGATTTCACCCGCTGTCTGAGAGGAACTGTGTATGCC	407
QY	156	AGAAGAAGTGAATTTCTTGGAAAAGATGAACATCCCAACATTTGAGCTTCTTCAAT	215
Db	408	TTGAATGAGATAGTATTCTTGGCACTGTCTGACAGCAGCAACATTTTGCCTACTACAT	467
QY	216	TCATTTCAAGAGAATGGCAGGCTGTTTATTGTAATGGAATATTGTGATGGAGGGATCTC	275
Db	468	CACCTCATGACAATACCACGCTGTGATTGAGCTGGAATATTGTAATGGAGGAACTG	527
QY	276	ATGAAAAGGATCAATAGACAACGGGGTGTGTTTATTAGTAGAGATCAGATCCTCGTTGG	335
Db	528	TATGACAAAATCCTTCGTGAGAGGACAAAGTGTGTTGAGGAAGAGATGCTGTGTGTAC	587
QY	336	TTTGTACAGATTTCTAGGACTTAAACATATTTCAATGACAGAGATATTACAGGGAC	395
Db	588	CTATTTCAAGATTTCTAGGACTTAAACATATTTCAATGACAGATATTACAGGGAT	647
QY	396	ATPAAAGCTCAGAACATTTTCTTACAGGAACGGAATGGTGGCAAGCTTTGGGGACCTT	455

Db 648 ATAAGACATTAATAATTTTCTGACCAAG--GCAACCTGATAAATCTGGAGATTAT 704
Qy 456 GGTATAGCAAGAGTCCTGAATAATTCATGGAACCTTGCTCGAACTTGTATTGGAACACCT 515
Db 705 GGCCTAGCAAGAAACTTAATCTGAGTATTCATGCTGAGACGCTTGTGGGAACCCCA 764
Qy 516 TACTACCTGCTCCAGAGATCTGTGAGATAAACCCTAGCAACAATAAAGCGGATTTGG 575
Db 765 TATTACATGCTCCAGAGCTCTGTCAAGAGTAAAGTACAAATTCAGTCTGATATCTGG 824
Qy 576 TCTCTTGCTGTGCTTATATGAGCTCTGCACACTTAAACATCCTTTGAGGGTAAACAAC 635
Db 825 GCAGTTGGCTGCTCAATTTTGAAGTCTTACCTTAAAGAGGAGCGTTGATGCTACAAAC 884
Qy 636 TTACAGAGCTGCTTGAAGATTGTCAGACACATTTTGGC 677
Db 885 CCACTTAACCTGTGTGCAAGATCGTCAAGGAATTCGGGCC 926

RESULT 14
US-09-544-794-8
; Sequence 8, Application US/09544794
; Patent No. 6541232
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Virca, G. Duke
; APPLICANT: Bird, Timothy A.
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: Polypeptides Having Kinase Activity
; FILE OF INVENTION: 2005-B
; CURRENT APPLICATION NUMBER: US/09/544,794
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 08/870,529
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/059,979
; PRIOR FILING DATE: 1996-06-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 3264
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-544-794-8

Query Match 7.0%; Score 166.8; DB 4; Length 3264;
Best Local Similarity 54.8%; Pred. No. 3.3e-38;
Matches 352; Conservative 0; Mismatches 287; Indels 3; Gaps 1;
Qy 36 GCCATCGGGGCAAGTGCCTTCGGGAAGCATACTTAGCTAAGGGAATCAGATAGCAAG 95
Db 288 GTCCTGGCCGCGCGCTTCGGGAAGCCACCGCTGTACCGCCGACCGAGGATGACTCA 347
Qy 96 CACTGTGTGTCATAAAGAGATCAATTTTGAAGAAGTGCCTATACAGAAAAGAAAGCTTCA 155
Db 348 CTGGTTGTGTGAGAGAGTGCATTTGACCGGCTGTCTGAGAGGAACCTGATGCC 407
Qy 156 AAGAAAGAGTGTCTTCTGGAAAGATGAACATCCCAACATTTAGCGCTTCTTCAAT 215
Db 408 TTGAATGAGATGATTTCTGGCACTGTGTCAGCAGCAGCAACATTTATGGCTACTACAAT 467
Qy 216 TCATTTCAAGAGATGGCAGCTGTTTATTTGTAATGGAATTTGTGATGAGGGGATCTC 275
Db 468 CACTTCATGGCAATACACCGCTGCTGATGAGCTGGAATTTGTATGAGGGAACCTG 527
Qy 276 ATGAAAGGATCAATAGACAAACGGGGTGTGTTATTTAGTGAAGATCAGATCCTCGGTGG 335
Db 528 TATGACAAAATCCCTCGTCAGAGGACAAAGTTGTTGAGGAAGAGATGGTGGTGTGCTAC 587
Qy 336 TTTGTACAGATTTCTTAGGACTAAACATATTTATGACAGGAAGATATTACACAGGAC 395
Db 588 CTATTTACAGATTTGTTGACGAGTGTGCTGATCCATTAAGCTGGAATCTCTTCATAGAT 647

Qy 396 ATAAAGCTCAGAACATTTTCTTAGCAAGAACGGAATGGTGCAAGCTTGGGACTTT 455
Db 648 ATAAAGCATTAATAATTTTCTGACCAAG---GCAACCTGATAAATCTGGAGATTAT 704
Qy 456 GGTATAGCAAGAGTCCTGAATAATTCATGGAACCTTGCTCGAACTTGTATTGGAACACCT 515
Db 705 GGCCTAGCAAGAAACTTAATCTGAGTATTCATGCTGAGACGCTTGTGGGAACCCCA 764
Qy 516 TACTACCTGCTCCAGAGATCTGTGAGATAAACCCTAGCAACAATAAAGCGGATTTGG 575
Db 765 TATTACATGCTCCAGAGCTCTGTCAAGAGTAAAGTACAAATTCAGTCTGATATCTGG 824
Qy 576 TCTCTTGCTGTGCTTATATGAGCTCTGCACACTTAAACATCCTTTGAGGGTAAACAAC 635
Db 825 GCAGTTGGCTGCTCAATTTTGAAGTCTTACCTTAAAGAGGAGCGTTGATGCTACAAAC 884
Qy 636 TTACAGAGCTGCTTGAAGATTGTCAGACACATTTTGGC 677
Db 885 CCACTTAACCTGTGTGGAAGATCGTCAAGGAATTCGGGCC 926

RESULT 15
US-10-196-927-3
; Sequence 3, Application US/10196927
; Patent No. 6797510
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Fiddle, Carl Johan
; TITLE OF INVENTION: No. 6797510el Human Kinases and Polynucleotides Encoding the Same
; FILE OF INVENTION: 2001-05-24
; CURRENT APPLICATION NUMBER: US/10/196,927
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 60/293,248
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1449
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-196-927-3

Query Match 5.6%; Score 131.6; DB 4; Length 1449;
Best Local Similarity 51.3%; Pred. No. 4.1e-28;
Matches 364; Conservative 0; Mismatches 334; Indels 12; Gaps 2;
Qy 102 GTCATAAAGAGATCAATTTTGAAGAAGTGCCTATACAGAAAAGAAAGCTTCAAGAAA 161
Db 175 GTACTTAAGGAATATCTGTTGGAGAACTAAATCCAAATGAATGTACAGGCCAATTG 234
Qy 162 GAAGTGATTTCTTGGAAAAGATGAACATCCCAACATTTAGCTTCTTCAATTCATTT 221
Db 235 GAAGCCCAACTCTCTCCCAAGCTGGACCCACCGCATTTGCAAGTTCCATGCAAGTTT 294
Qy 222 CAAGAGATGGCAGCTGTTTATTGTAATGGAATTTGATGAGGGGGATCTCATGAAA 281
Db 295 GTGAGCAAGATAATTTCTGCATTAACGGAGTACTGTGAGGGCCGAGATCTGGACGAT 354
Qy 282 AGGATCA-----ATAGACAACGGGGTGTGTTATTAGTGAAGATCAGATCCTCGGTGG 335
Db 355 AAAATTTCAGGAATATAAACAAGCTGGAATAATCTTCCAGAAAATCAAAATTAATAGAATGG 414
Qy 336 TTTGTACAGATTTCTTAGGACTAAACATATTATGATGACAGGAAGATATTACAGGGAC 395
Db 415 TTTATCCAGCTCTCTGGAGTTGCTACATGATGATGAGAGGAGATATTCAATCGAGAC 474
Qy 396 ATAAAGCTCAGAACATTTTCTTAGCAAGAACCGGAATGGTGGCAAGCTTGGGACTTT 455
Db 475 TTAAGTCAAGAATGTTTCTGAAAAATAA-----TCTCTTAAATTTGGAGATT 528
Qy 456 GGTATAGCAAGAGTCTCTGAATAATTTCCATGGAATTTGCTCGAATTTGTTGGAAACACT 515

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Db 529 GGAGTTTCTCGATTCTAATGGGATCCTGTGACCTGGCCACAACTTTAACTGGAACTCCC 588
QY 516 TACTACCTGTCCCGAGAGATCTGTGAGAAATAAACCCCTACACAAATAAAACCGGATATTTGG 575
Db 589 CATTATATGAGTCTCTGAGGCTCTGAAACACCAAGGCTATGACACAAAGTCGGACATCTGG 648
QY 576 TCTCTTGGCTGTCTTATATGAGCTCTGCACACTTAAACATCCCTTTGAGGGTAAACAAC 635
Db 649 TCACCTGGCATGCAATTTGTATGAGATGTGCTGCATGAATCATGCAATTCGCTGGCTCCAAT 708
QY 636 TTACAGCAGCTGGTCTGGAAGATTTGTCAAGCACATTTTGGCCCAATATCTCCGGGGTTT 695
Db 709 TTCTTATCCATTGTTTAAATTTGTTGAGGTGACACACCTTCTCTCCCTGAGAGATAT 768
QY 696 TCTCGTGAGCTCCATTCCCTTGATATCTGAGCTCTTTCAAGTATCTCCTCGAGACCGACCA 755
Db 769 CCAAAAGAACTAAATGCCATCATGGAAGCATGTTGAACAGAAATCCTTCATTAAGACCA 828
QY 756 TCCATAAATTCATTTTGAAGGCCCTTTTATAGAGAAATCTTTATCCCAA 805
Db 829 TCTGCTATCGAAATTTTAAATTCCTTACCTTGATGACGAGTACAGAA 878

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Search completed: November 8, 2004, 02:03:08
 Job time : 222 secs

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Result No.	Score	Query Match	Length	DB ID	Description
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	Query Match	100.0%;	Score 2370;	DB 14;	Length 2370;	
	Best Local Similarity	100.0%;	Pred. No. 0;			
	Matches 2370;	Conservative	0;	Mismatches	0;	Indels
						Gaps
						0;
Qy	1	CATTGAGACCATGGATAAGTACCGATGTGATTAAAGCCATCGGGCAAGTGCCCTTCGGGA	60			
Db	1	CATTGAGACCATGGATAAGTACCGATGTGATTAAAGCCATCGGGCAAGTGCCCTTCGGGA	60			
Qy	61	AAGCATACTTAGCTAAAGGGAATCAGATGACGACACTGTGTCTATAAAGAGATCAATT	120			
Db	61	AAGCATACTTAGCTAAAGGGAATCAGATGACGACACTGTGTCTATAAAGAGATCAATT	120			
Qy	121	TTGAAAAGATGCCCATACAAGAAAAAGAGCTTCAAGAAAAAGAGTGATCTTCTCGAAA	180			
Db	121	TTGAAAAGATGCCCATACAAGAAAAAGAGCTTCAAGAAAAAGAGTGATCTTCTCGAAA	180			

181 QY AGATGAACATCCCAACATTTGAGCTCTTCAATTCATTTCAAGAGATGGCAGCTGT 240
181 Db AGATGAACATCCCAACATTTGAGCTCTTCAATTCATTTCAAGAGATGGCAGCTGT 240
241 QY TTATTTGTAATGGAATATTTGATGGAGGATCTCATGAAAGGATCAATAGACACGG 300
241 Db TTATTTGTAATGGAATATTTGATGGAGGATCTCATGAAAGGATCAATAGACACGG 300
301 QY GTGTGTTATTTAGTGAAGATCAGATCCTCGTTGGTTTGTACAGATTTCTTAGGACTAA 360
301 Db GTGTGTTATTTAGTGAAGATCAGATCCTCGTTGGTTTGTACAGATTTCTTAGGACTAA 360
361 QY AACATATTCATGACAGGAAGATATTACAGAGGACATATAAAGCTCAGACATTTTCTTA 420
361 Db AACATATTCATGACAGGAAGATATTACAGAGGACATATAAAGCTCAGACATTTTCTTA 420
421 QY GCAGAACGGATGGTGCAGGCTTGGGACCTTGGTATAGCAAGAGCTCCTGAATTA 480
421 Db GCAGAACGGATGGTGCAGGCTTGGGACCTTGGTATAGCAAGAGCTCCTGAATTA 480
481 QY CCATGGAACCTTGCCTGAACTTGTATTGGAACACCTTACTACCTGTCCCGAGAGATCTGTC 540
481 Db CCATGGAACCTTGCCTGAACTTGTATTGGAACACCTTACTACCTGTCCCGAGAGATCTGTC 540
541 QY AGATTAACCTTACCAATTAACCGATATTTGGTCTCTGGCTGTCTTATATGAGC 600
541 Db AGATTAACCTTACCAATTAACCGATATTTGGTCTCTGGCTGTCTTATATGAGC 600
601 QY TCTGCACACTTAAACATCTTTGAGGTTAAACCTTACAGAGCTGGTTCTGAAGATTT 660
601 Db TCTGCACACTTAAACATCTTTGAGGTTAAACCTTACAGAGCTGGTTCTGAAGATTT 660
661 QY GTCCAGACATTTGGCCCAATATCTCCGGGTTTCTCGTGAGCTCCATTCCTTCATAT 720
661 Db GTCCAGACATTTGGCCCAATATCTCCGGGTTTCTCGTGAGCTCCATTCCTTCATAT 720
721 QY CTCAGCTCTTCAAGTATCTCTCGAGACCGACCATCCATAAATTCATTTGAAAGGC 780
721 Db CTCAGCTCTTCAAGTATCTCTCGAGACCGACCATCCATAAATTCATTTGAAAGGC 780
781 QY CTTTTTAGAGATCTTTATTTCCCAATATTTGATCTCTGAGGTCATTCAGGAAGATTTCA 840
781 Db CTTTTTAGAGATCTTTATTTCCCAATATTTGATCTCTGAGGTCATTCAGGAAGATTTCA 840
841 QY GTCCATGCTTATATGAGAGCGGCGCCAGCTTCTCGACATGCTGGAGAGTGGTCC 900
841 Db GTCCATGCTTATATGAGAGCGGCGCCAGCTTCTCGACATGCTGGAGAGTGGTCC 900
901 QY AGAAGTGTAAATACAAAAAGTGAGATTCGCGGGAAGTGCCCAACCAAGATCAAGGATAT 960
901 Db AGAAGTGTAAATACAAAAAGTGAGATTCGCGGGAAGTGCCCAACCAAGATCAAGGATAT 960
961 QY CTGTGCCAATTAAGGAATGCTATATTGATAGAAATGATGAGACCAACAGCTGGAG 1020
961 Db CTGTGCCAATTAAGGAATGCTATATTGATAGAAATGATGAGACCAACAGCTGGAG 1020
1021 QY CCCAGAGGCGCAGATCTATAAATATAGAAAGACCCAAATTTGCTGTGCTGTGGAC 1080
1021 Db CCCAGAGGCGCAGATCTATAAATATAGAAAGACCCAAATTTGCTGTGCTGTGGAC 1080
1081 QY ATTTAGATTTATTTGCTCAACTTGTATGCTGAGGAGAGGCCCAACCAAGTT 1140
1081 Db ATTTAGATTTATTTGCTCAACTTGTATGCTGAGGAGAGGCCCAACCAAGTT 1140
1141 QY ATCCCTTATTCCTCAAGAAATATCTGGAGTTAGAGATTTACGGTCAAGAAACAGGCGATG 1200
1141 Db ATCCCTTATTCCTCAAGAAATATCTGGAGTTAGAGATTTACGGTCAAGAAACAGGCGATG 1200
1201 QY GTCCATCCCAAGTCAATGGCTGCTGAGTACCTTTCAGAGAAATTTGAAGCTCAACAT 1260
1201 Db GTCCATCCCAAGTCAATGGCTGCTGAGTACCTTTCAGAGAAATTTGAAGCTCAACAT 1260

1261 QY ATAAAGTTGAAAGTGGAGAACCAATTTGGTCTTGGTCCATCTTTCTGCCGAGCCAAATTACA 1320
1261 Db ATAAAGTTGAAAGTGGAGAACCAATTTGGTCTTGGTCCATCTTTCTGCCGAGCCAAATTACA 1320
1321 QY ACCAGAGACAGAGCTTAAGAGTAATGGAGAGAGCTAGATTTCCAGGAGCTGCCATTTA 1380
1321 Db ACCAGAGACAGAGCTTAAGAGTAATGGAGAGAGCTAGATTTCCAGGAGCTGCCATTTA 1380
1381 QY GGAAAAACGAAATGAAGAACACAGGAATATTGGAAAGCTTTAGAGAAATACGCCAACAGT 1440
1381 Db GGAAAAACGAAATGAAGAACACAGGAATATTGGAAAGCTTTAGAGAAATACGCCAACAGT 1440
1441 QY ACCTCAATGACATCAAGAAATTAAGAAAGATGGGGAGAGAACACAGAGACATTTGAAA 1500
1441 Db ACCTCAATGACATCAAGAAATTAAGAAAGATGGGGAGAGAACACAGAGACATTTGAAA 1500
1501 QY AAGACTTTGAAAACAAATGAGGCTTCAGAACACAAAGGAAAGTAAAAATCCAGAACAGAAAT 1560
1501 Db AAGACTTTGAAAACAAATGAGGCTTCAGAACACAAAGGAAAGTAAAAATCCAGAACAGAAAT 1560
1561 QY ATAAAGCTTAAGAGGGGTAAAAATTTGAATTAATTTAGACAAATGATTTCTGATGAAA 1620
1561 Db ATAAAGCTTAAGAGGGGTAAAAATTTGAATTAATTTAGACAAATGATTTCTGATGAAA 1620
1621 QY ACATCCTCCAAAGAGAGAGGCAATGGATATACCAAAATGAAACTTTGACCTTTGAGGATG 1680
1621 Db ACATCCTCCAAAGAGAGAGGCAATGGATATACCAAAATGAAACTTTGACCTTTGAGGATG 1680
1681 QY GCATGAAGTTTAAGGAATATGAATGTTAAAGGAGCATGGAGATTATACAGACAAAGCAT 1740
1681 Db GCATGAAGTTTAAGGAATATGAATGTTAAAGGAGCATGGAGATTATACAGACAAAGCAT 1740
1741 QY TTGAAAAACTTCACTGCCAGAACAGCAATTTACAGAACTGACTTGGCTCAGTTTCTCT 1800
1741 Db TTGAAAAACTTCACTGCCAGAACAGCAATTTACAGAACTGACTTGGCTCAGTTTCTCT 1800
1801 QY TCCTGGAAATATCTCTGCTCATTTTCTCGGAAAAATCTCCATTCAGCAGGATCTTA 1860
1801 Db TCCTGGAAATATCTCTGCTCATTTTCTCGGAAAAATCTCCATTCAGCAGGATCTTA 1860
1861 QY TTGAGGATCTCTTTGTCGCAACGACTGCTCACTGAAAGGCTGGAGTGAGAGAAATGG 1920
1861 Db TTGAGGATCTCTTTGTCGCAACGACTGCTCACTGAAAGGCTGGAGTGAGAGAAATGG 1920
1921 QY AGCTTAGGACATAACCTTACCCTTACCACTACATAAACAACCTTTGGAGAAATCAGGAGAGTAAA 1980
1921 Db AGCTTAGGACATAACCTTACCCTTACCACTACATAAACAACCTTTGGAGAAATCAGGAGAGTAAA 1980
1981 QY GCCAAAGAGAGAGACAGATCATGGGAGGACACAGGAATGGCAGCATCAACTGGAGAA 2040
1981 Db GCCAAAGAGAGAGACAGATCATGGGAGGACACAGGAATGGCAGCATCAACTGGAGAA 2040
2041 QY GAAAGGCCAGATGAGGGTTTTCCACGAGACTGTAGTTGTCTGTGGGAAACAGGAGGAGT 2100
2041 Db GAAAGGCCAGATGAGGGTTTTCCACGAGACTGTAGTTGTCTGTGGGAAACAGGAGGAGT 2100
2101 QY GGGATGGAGAGCGCTCAGACTCTGCTGAGATGATGGCAGTGGCCGACATCACTTCCA 2160
2101 Db GGGATGGAGAGCGCTCAGACTCTGCTGAGATGATGGCAGTGGCCGACATCACTTCCA 2160
2161 QY CCTGCCCCACGGGCTCAGACTGTGCTTGTAGTGTGCTTGTGCTGAGGAAAGGAGAA 2220
2161 Db CCTGCCCCACGGGCTCAGACTGTGCTTGTAGTGTGCTTGTGCTGAGGAAAGGAGAA 2220
2221 QY CCAAGGACCCGTACAGCCAGTGTCTATCTGATGATGATGATCTTCTCATCTATACAC 2280
2221 Db CCAAGGACCCGTACAGCCAGTGTCTATCTGATGATGATGATCTTCTCATCTATACAC 2280
2281 QY CCTATAGATCTTGTATCAGACACTTTCAAAATATGCTGTTTTGTATATCTCAAGAAAAAAA 2340
2281 Db CCTATAGATCTTGTATCAGACACTTTCAAAATATGCTGTTTTGTATATCTCAAGAAAAAAA 2340
2341 QY AAAAAAACACTGTCTATGCCCTTACGAGCG 2370

QY 1141 ATCACCTTCTCTCAAGAAATACCTGGATTGAGATTACGGTCAGGAAACGAGGCATG 1200
 Db 1234 ATCACCTTCTCTCAAGAAATACCTGGATTGAGATTACGGTCAGGAAACGAGGCATG 1293
 QY 1201 GTCCATCCCAAGTCAATGSCCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACAT 1260
 Db 1294 GTCCATCCCAAGTCAATGSCCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACAT 1353
 QY 1261 ATAAGTTGAAGTGGAGAACCAATTTGGTCTTCATCTTCTGCGAGCCAAATTACA 1320
 Db 1354 ATAAGTTGAAGTGGAGAACCAATTTGGTCTTCATCTTCTGCGAGCCAAATTACA 1413
 QY 1321 ACCAGAGACAAAGAGCTTAAGAGTAATGGAGAGAGCTAGATTCCAGGAGCTGCCATTTA 1380
 Db 1414 ACCAGAGACAAAGAGCTTAAGAGTAATGGAGAGAGCTAGATTCCAGGAGCTGCCATTTA 1473
 QY 1381 GGAAGAAACGAATGAAGGAAACAGGAATATTGGAGAGCTTTAGAGGAAATACGCCAACAT 1440
 Db 1474 GGAAGAAACGAATGAAGGAAACAGGAATATTGGAGAGCTTTAGAGGAAATACGCCAACAT 1533
 QY 1441 ACCTCAATGACATGAAGAAATTTAGAAAGAGATGGGAGAGAACCCAG----- 1488
 Db 1534 ACCAATGACATGAAGAAATTTAGAAAGAGATGGGAGAGAACCCAGAGGAGAACTCAA 1593
 QY 1489 ----- 1488
 Db 1594 AAATAAGTCATAAAACCTATTGGTGAAGAGAGTAACTGCTGCTCCATCAAGATGCAT 1653
 QY 1489 -----AGGACATTGAAGAAAGACTTGAACAAATGAGCTTCAGA 1527
 Db 1654 CTGAGGAGAGCACTGTGCGAGGACATTGAAAGAGCTTGAACAAATGAGCTTCAGA 1713
 QY 1528 ACACAAAGGAAAGTAAAAATCCAGAAACAGAAATATAAAGCTTAAGAGGGGGTAAAAATTG 1587
 Db 1714 ACACAAAGGAAAGTAAAAATCCAGAAACAGAAATATAAAGCTTAAGAGGGGGTAAAAATTG 1773
 QY 1588 AAATTAATTTAGACAAATGATTTCTGATGAAGAAACATCTCCAGAGGAGGGAATG 1647
 Db 1774 AAATTAATTTAGACAAATGATTTCTGATGAAGAAACATCTCCAGAGGAGGGAATG 1833
 QY 1648 ATATACCAATGAACTTTGACCTTTGAGGATGCAATGAAGTTTAAGGAATATGAATGTG 1707
 Db 1834 ATATACCAATGAACTTTGACCTTTGAGGATGCAATGAAGTTTAAGGAATATGAATGTG 1893
 QY 1708 TAAAGGAGCATGAGATTTATACAGAAAGCAATTTGAAAGAACTTCACTCCAGAGAGCAG 1767
 Db 1894 TAAAGGAGCATGAGATTTATACAGAAAGCAATTTGAAAGAACTTCACTCCAGAGAGCAG 1953
 QY 1768 CATTTACAGAACTGACT 1784
 Db 1954 GGTTCCTCCAGCAGACT 1970

RESULT 4

US-10-618-941-28
 ; Sequence 28, Application US/10618941
 ; Publication No. US2004019792A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WHYTE, DAVID
 ; APPLICANT: MANNING, GERARD
 ; APPLICANT: CAENPEPEL, SEAN
 ; TITLE OF INVENTION: NOVEL KINASES
 ; FILE REFERENCE: 034536-0321
 ; CURRENT APPLICATION NUMBER: US/10/618,941
 ; CURRENT FILING DATE: 2003-07-15
 ; PRIOR APPLICATION NUMBER: 60/395,632
 ; PRIOR FILING DATE: 2002-07-15
 ; NUMBER OF SEQ ID NOS: 143
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 28
 ; LENGTH: 2816
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-10-618-941-28
 Query Match 70.3%; Score 1665; DB 18; Length 2816;
 Best Local Similarity 94.5%; Pred. No. 0;
 Matches 1774; Conservative 0; Mismatches 10; Indels 93; Gaps 1;
 QY 1 CATTGGAGACCATGGATAAGTACGATGTGATTAAAGGCCATCGGGCAAGGTCCTTCGGGA 60
 Db 307 CATTGGAGACCATGGATAAGTACGATGTGATTAAAGGCCATCGGGCAAGGTCCTTCGGGA 366
 QY 61 AAGCATCTTACGTAAAGGGAAATCAGATAGCAAGCACTGTGTCTATAAAGAGATCAATT 120
 Db 367 AAGCATCTTACGTAAAGGGAAATCAGATAGCAAGCACTGTGTCTATAAAGAGATCAATT 426
 QY 121 TTGAAAAGATGCCCATACAGAAAAGAGCTTCARAAAGAGAGTCAATCTTCGAAA 180
 Db 427 TTGAAAAGATGCCCATACAGAAAAGAGCTTCARAAAGAGAGTCAATCTTCGAAA 486
 QY 181 AGATGAACATCCCAACATTTAGCCTTTCTCAATTTCAATTTCAAGAGAAATGGCAGGTGT 240
 Db 487 AGATGAACATCCCAACATTTAGCCTTTCTCAATTTCAATTTCAAGAGAAATGGCAGGTGT 546
 QY 241 TTATTGTAATCGAATATTGTGATGGAGGGATCTCATGAAAAGGATCAATAGACAACGGG 300
 Db 547 TTATTGTAATCGAATATTGTGATGGAGGGATCTCATGAAAAGGATCAATAGACAACGGG 606
 QY 301 GTGTGTTATTTAGTGAAGATCAGATCTCGGTTGGTTGTACAGATTTCTCTAGGACTAA 360
 Db 607 GTGTGTTATTTAGTGAAGATCAGATCTCGGTTGGTTGTACAGATTTCTCTAGGACTAA 666
 QY 361 AACATTTTCATGACAGGAAGATATTACACAGGACATAAAGCTCAGAACATTTTCTTA 420
 Db 667 AACATTTTCATGACAGGAAGATATTACACAGGACATAAAGCTCAGAACATTTTCTTA 726
 QY 421 GCAAGACGGAATGCTGCAAGCTTTGGGACTTTGGTATAGCAAGAGTCTGTAATATT 480
 Db 727 GCAAGACGGAATGCTGCAAGCTTTGGGACTTTGGTATAGCAAGAGTCTGTAATATT 786
 QY 481 CCATGGAATTTGCTCGAACTTTGTAATGGAAACACCTTACTACCTGTCCTCCAGAGATCTGTC 540
 Db 787 CCATGGAATTTGCTCGAACTTTGTAATGGAAACACCTTACTACCTGTCCTCCAGAGATCTGTC 846
 QY 541 AGAATTAACCTTACACAAATAAAGGATATTGGTCTCTGGCTGTGTCTTATATAGC 600
 Db 847 AGAATTAACCTTACACAAATAAAGGATATTGGTCTCTGGCTGTGTCTTATATAGC 906
 QY 601 TCTGCACACTTAAACATCTTTTGGAGGTAAACAACTTACAGCAGCTGGTCTGAAGATTT 660
 Db 907 TCTGCACACTTAAACATCTTTTGGAGGTAAACAACTTACAGCAGCTGGTCTGAAGATTT 966
 QY 661 GTCAAGACATTTTGGCCCCAATATCTCGGGGTTTTCTCGTGGCTCATTCCTTGATAT 720
 Db 967 GTCAAGACATTTTGGCCCCAATATCTCGGGGTTTTCTCGTGGCTCATTCCTTGATAT 1026
 QY 721 CTCAGCTCTTTCAAGTATCTCTCGAGACCGACCATCCATAAATTCATTTTGAAGGC 780
 Db 1027 CTCAGCTCTTTCAAGTATCTCTCGAGACCGACCATCCATAAATTCATTTTGAAGGC 1086
 QY 781 CCTTTTATAGAAATCTTATTTCCCAATATTGACTCTCTGAGGTCAATTCAGAGAAATCA 840
 Db 1087 CCTTTTATAGAAATCTTATTTCCCAATATTGACTCTCTGAGGTCAATTCAGAGAAATCA 1146
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 Db 1147 GTCACATGCTTATATGACAGCAGAGCGCCAGCTTCTCGACATGCTGGGAGGTGCTCC 1206
 QY 901 AGAAGTGTAAATACAAAAGTGAATTTCCGGGAAAGTGCCTCCACCAAGATCAAGGATAT 960
 Db 1207 AGAAGTGTAAATACAAAAGTGAATTTCCAGGAAAGTGCCTCCACCAAGATCAAGGATAT 1266
 QY 961 CTGTGCCAATTAAGAGATCTATATTGCAATAGAAATGAATGGAGACCAACAGCTGAG 1020
 Db 1267 CTGTGCCAATTAAGAGATCTATATTGCAATAGAAATGAATGGAGACCAACAGCTGAG 1326

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QY 1021 CCCAGAGCCAGATCTATAAAATGATAGAAAGCCAAATTTGCTGCTCTCTGTGGAC 1080
Db 1327 CCCAGAGCCAGATCTATAAAATGATAGAAAGCCAAATTTGCTGCTCTCTGTGGAC 1386
QY 1081 ATTATGATTATTATTATGCTCAACTTGTATGCTGAGGAGAGAGCCACAAACCAAGTT 1140
Db 1387 ATTATGATTATTATTATGCTCAACTTGTATGCTGAGGAGAGAGCCACAAACCAAGTT 1446
QY 1141 ATCACCTTATCTCAAGAAATATCTGGAGTTGAGGATTACGGTCAGAAACGAGGATG 1200
Db 1447 ATCACCTTATCTCAAGAAATATCTGGAGTTGAGGATTACGGTCAGAAACGAGGATG 1506
QY 1201 GTCATCCCGCAATCAATGGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 1260
Db 1507 GTCATCCCGCAATCAATGGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 1566
QY 1261 ATAAGTTGAAAGTGAGAGCAATTTGGGTCTTTCGTCATCTTCTGCCGAGCCAAATTA 1320
Db 1567 ATAAGTTGAAAGTGAGAGCAATTTGGGTCTTTCGTCATCTTCTGCCGAGCCAAATTA 1626
QY 1321 ACCAGAGACAGAGCTAAGAGTAATGAGAGAGAGCTTAGATTTCCAGAGCTGCCATT 1380
Db 1627 ACCAGAGACAGAGCTAAGAGTAATGAGAGAGAGCTTAGATTTCCAGAGCTGCCATT 1686
QY 1381 GGAAGAAACGAATGAAGCAAGCAATTTGGAAGCAGTTAGAGGAATACGCCAACAGT 1440
Db 1687 GGAAGAAACGAATGAAGCAAGCAATTTGGAAGCAGTTAGAGGAATACGCCAACAGT 1746
QY 1441 ACCTCAATGACATGAAGAAATATGAAAGAGAGTGGGAGAGAACCCAG - 1488
Db 1747 ACCAATGACATGAAGAAATATGAAAGAGAGTGGGAGAGAACCCAGAGAGGAACCT 1806
QY 1489 ----- 1488
Db 1807 AATTAAGTCATAAACCTATTGTTGTAAGAGAGTAACCTGCTGTCATCAAGATGCAT 1866
QY 1489 -----AGGCAATTGAAAGAGCTTGAAACAAATGAGGCTTCAGA 1527
Db 1867 CTGAGGGAGAGCACCCTGTGAGGAGACTTGAAAGAGCTTGAAACAAATGAGGCTTCAGA 1926
QY 1528 ACACAAAGGAAGTAATAATCCAGACAGATATTAAGCTTAAGAGAGGGGTAAATTTG 1587
Db 1927 ACACAAAGGAAGTAATAATCCAGACAGATATTAAGCTTAAGAGAGGGGTAAATTTG 1986
QY 1588 AAATTAATTTAGACAAATGTATTTCTGATGAAACATCTCCAGAGAGAGAGGCAATGG 1647
Db 1987 AAATTAATTTAGACAAATGTATTTCTGATGAAACATCTCCAGAGAGAGAGGCAATGG 2046
QY 1648 ATATACCAATGAACCTTTGACCTTTGAGGATGGATGAAGTTTAAGGAATATGAATGG 1707
Db 2047 ATATACCAATGAACCTTTGACCTTTGAGGATGGATGAAGTTTAAGGAATATGAATGG 2106
QY 1708 TAAAGGACATGGAGATTATACAGACAAAGCAATTTGAAACACTTCACTGCCAGAGCAG 1767
Db 2107 TAAAGGACATGGAGATTATACAGACAAAGCAATTTGAAACACTTCACTGCCAGAGCAG 2166
QY 1768 CATTTCAGAACTGACT 1784
Db 2167 GGTTCACGAGACT 2183
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RESULT 5

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US-09-940-921B-3
; Sequence 3, Application US/09940921B
; Patent No. US20020147320A1
; GENERAL INFORMATION:
; APPLICANT: Fiddle, Carl Johan
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: No. US20020147320A1 Human Kinase Proteins and Polynucleotides
; FILE REFERENCE: LEX-0227-USA
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; CURRENT APPLICATION NUMBER: US/09/940,921B
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/229,280
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1965
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-940-921B-3
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Query Match 69.9%; Score 1656.2; DB 9; Length 1965;

Best Local Similarity 96.1%; Pred. No. 0; Mismatches 63; Indels 6; Gaps 1;
Matches 1710; Conservative 0;

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QY 12 ATGGATAAGTACGATGTGATTAAAGCCATCGGCAAGTGCCTTCGGAAAGCATACTTA 71
Db 1 ATGGATAAGTACGATGTGATTAAAGCCATCGGCAAGTGCCTTCGGAAAGCATACTTA 60
QY 72 GCTAAAGGAAATCAGATAGCAGCACTCTGTGCATATAAGAGATCAATTTTGAAGATG 131
Db 61 GCTAAAGGAAATCAGATAGCAGCACTCTGTGCATATAAGAGATCAATTTTGAAGATG 120
QY 132 CCATACAAGAAAGAAAGCTTCAAGAAAGAGTATTCTTCTGAAAGATGAACAT 191
Db 121 CCATACAAGAAAGAAAGCTTCAAGAAAGAGTATTCTTCTGAAAGATGAACAT 180
QY 192 CCCAATTTGAGCTTCTTCAATTCATTTCAAGAGATGGCAGCTGTATTGTAATG 251
Db 181 CCCAATTTGAGCTTCTTCAATTCATTTCAAGAGATGGCAGCTGTATTGTAATG 240
QY 252 GAATATTGTGAGGGGATCTCATGAAAGAGTCAATAGACAAAGGGGTGTGTTATT 311
Db 241 GAATATTGTGAGGGGATCTCATGAAAGAGTCAATAGACAAAGGGGTGTGTTATT 300
QY 312 AGTGAAGATCAGATCCTCGTGGTTGTACAGATTTCTAGGACTAAGACATATTTCAT 371
Db 301 AGTGAAGATCAGATCCTCGTGGTTGTACAGATTTCTAGGACTAAGACATATTTCAT 360
QY 372 GACAGAGATATACACAGGAGACATAAAGCTCAGAACATTTTCTTAGCAAGACGGA 431
Db 361 GACAGAGATATATACACAGGAGACATAAAGCTCAGAACATTTTCTTAGCAAGACGGA 420
QY 432 ATGTTGGCAAGACTTTGGGACTTTTGGTATAGCAAGAGTCTTGAATTAATTCATG 491
Db 421 ATGTTGGCAAGACTTTGGGACTTTTGGTATAGCAAGAGTCTTGAATTAATTCATG 480
QY 492 GCTCGAATTTGTTGGACACCTTACTACCTGTCGCCAGAGATCTGTCAGATTAACCC 551
Db 481 GCTCGAATTTGTTGGACACCTTACTACCTGTCGCCAGAGATCTGTCAGATTAACCC 540
QY 552 TACAACATATAAAGAGATTTTGGTCTCTTGGCTGTGCTTATATGAGCTCTGCACTT 611
Db 541 TACAACATATAAAGAGATTTTGGTCTCTTGGCTGTGCTTATATGAGCTCTGCACTT 600
QY 612 AAACATCTTTTGGAGGTAAACATTCAGAGCTGGTTCTGAAAGATTTGTCAGACAT 671
Db 601 AAACATCTTTTGGAGGTAAACATTCAGAGCTGGTTCTGAAAGATTTGTCAGACAT 660
QY 672 TTTGCCCAATATCTCCGGGGTTTTCTGCTGAGCTCCATTCCTTCATATCTCAGCTCTT 731
Db 661 TTTGCCCAATATCTCCGGGGTTTTCTGCTGAGCTCCATTCCTTCATATCTCAGCTCTT 720
QY 732 CAAGTATCTCTCGAGACCGACCATCCATAAATTCATTTGAAAGGCCCTTTTAGAG 791
Db 721 CAAGTATCTCTCGAGACCGACCATCCATAAATTCATTTGAAAGGCCCTTTTAGAG 780
QY 792 AATCTTATTTCCCAATATTTGACTCTCTCAGGTTCATTTCAGGAAGAAATTCAGTCA 851
Db 781 AATCTTATTTCCCAATATTTGACTCTCTCAGGTTCATTTCAGGAAGAAATTCAGTCA 840
QY 852 ATATGAGAGCAGGAGCCGCCAGTCTTCGACATGCTGGGAAGGGTTCAGGAAGTGA 911
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Db 841 ATATGCAGAGCAGGAGCGCCAGCTTCTCGACATGCTGGGAAGTGGTCCAGAAGTGTAAA 900
QY 912 ATACAAAAAGTGCAGATTCGGGGAAGTCCCAACCAAGATCAAGGATATCTGTGCAATT 971
Db 901 ATACAAAAAGTGCAGATTCGGGGAAGTCCCAACCAAGATCAAGGATATCTGTGCAATT 960
QY 972 AAAAGGAATGCTATATTCATAGAAATGAATGGAGACCAACAGCTGGAGCCAGAGGCC 1031
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QY 1032 AGATCTATAAAATGATAGAAAGCCAAAATTTGCTGCTGTCTGTGGACATTAATGATTAT 1091
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QY 1092 TATTATGCTCAACTGATATGCTGAGGAGAGGCCCAACCAAGTTATCACCTTAT 1151
Db 1081 TATTATGCTCAACTGATATGCTGAGGAGAGGCCCAACCAAGTTATCACCTTAT 1140
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Db 1141 CCTCAAGAAAATACTCGAGTTAGGATTAAGGTTCAGAAAACAGGAGCATGGTCCATCCCA 1200
QY 1212 AGTCAATGGCTGCTGAGTACCTTCAGAGAAAATTTGAAGTCAACAAATATAGTTGAAA 1271
Db 1201 AGTCAATGGCTGCTGAGTACCTTCAGAGAAAATTTGAAGTCAACAAATATAGTTGAAA 1260
QY 1272 GTGAGAGCAATTTGGTCTCTGCTCCATCTTCTGCCGAGCCAAATTTACAAACAGAGACA 1331
Db 1261 GTGAGAGCAATTTGGTCTCTGCTCCATCTTCTGCCGAGCCAAATTTACAAACAGAGACA 1320
QY 1332 GAGCTAAGAGTAATGGAGAAAGCCTAGATTTCCAGGAGCTGCAATTTAGGAAAACGAA 1391
Db 1321 GAGCTAAGAGTAATGGAGAAAGCCTAGATTTCCAGGAGCTGCAATTTAGGAAAACGAA 1380
QY 1392 ATGAGGAACAGGAATATTTGGAAGCAGTTAGAGGAATATAGCCACAGTACCTCATGAC 1451
Db 1381 ATGAGGAACAGGAGAACTCAAAAATAAGTCAATAAAACCTATTGTGTGAAGAAGTAAC 1440
QY 1452 ATCAAGAAATTTAGAAAGAGATGGGAGAGAACCA-----GAGGACATTTGAAAAGAC 1505
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Db 1501 TTGAAAACAAATGAGCTTCAGAACACAAAGGAAGTAAAAATCCAGAAACAGAAATATAA 1560
QY 1566 GCTAAGAGGGGTAAATTTGAAATTAATTTAGACAAATGTATTTCTGATGAAAACATC 1625
Db 1561 GCTAAGAGGGGTAAATTTGAAATTAATTTAGACAAATGTATTTCTGATGAAAACATC 1620
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Db 1621 CTCGAAGAGGAGGCAATGGATATACCAATGAAACTTTGACCTTTGAGGATGGCATG 1680
QY 1686 AAGTTTAAGGAATATGAATGTGTAAGGAGCATGGAGATTATACAGACAAGCAATTTGAA 1745
Db 1681 AAGTTTAAGGAATATGAATGTGTAAGGAGCATGGAGATTATACAGACAAGCAATTTGAA 1740
QY 1746 AACTTTCACCTGCCGAGAGCAGCATTTACAGAACTGACT 1784
Db 1741 AACTTTCACCTGCCGAGAGCAGGGTTTCCACGCAGACT 1779

RESULT 6
US-09-940-921B-1
; Sequence 1, Application US/09940921B
; Patent No. US20020147320A1
; GENERAL INFORMATION:
; APPLICANT: Fiddle, Carl Johan
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Hu, Yi

; TITLE OF INVENTION: No. US20020147320A1el Human Kinase Proteins and Polynucleotides E
; FILE REFERENCE: LEX-0227-USA
; CURRENT APPLICATION NUMBER: US/09/940,921B
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/229,280
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2052
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-940-921B-1

Query March 69.8%; Score 1654; DB 9; Length 2052;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 1763; Conservative 0; Mismatches 10; Indels 93; Gaps 1;

QY 12 ATGATAAGTACGATGTGATTAAAGCCATCGGCAAGTGCCTTCGGAAAGCATACTTA 71
Db 1 ATGATAAGTACGATGTGATTAAAGCCATCGGCAAGTGCCTTCGGAAAGCATACTTA 60
QY 72 GCTAAAGGAAATCAGATAGCAAGCACTGTGTCATAAAGAGATCAATTTGAAAAGATG 131
Db 61 GCTAAAGGAAATCAGATAGCAAGCACTGTGTCATAAAGAGATCAATTTGAAAAGATG 120
QY 132 CCCATACAAGAAAAAGAGCTTCAAGAAAGAAAGTGTCTTCTGGAAGAGATCAACAT 191
Db 121 CCCATACAAGAAAAAGAGCTTCAAGAAAGAAAGTGTCTTCTGGAAGAGATCAACAT 180
QY 192 CCCAACATGTAGGCTTCTCAATTCATTTCAAGAGAAATGCGAGGCTGTTATTGTAATG 251
Db 181 CCCAACATGTAGGCTTCTCAATTCATTTCAAGAGAAATGCGAGGCTGTTATTGTAATG 240
QY 252 GAATATTGTGATGAGGGGATCTCATGAAAAGATCAATAGACAAACGGGTGTCTTATTT 311
Db 241 GAATATTGTGATGAGGGGATCTCATGAAAAGAGTCAATAGACAAACGGGTGTCTTATTT 300
QY 312 AGTGAAGATCAGATCCTCGSTTGGTTTGTACAGATTTCTCTAGGACTTAAACATATTCAAT 371
Db 301 AGTGAAGATCAGATCCTCGSTTGGTTTGTACAGATTTCTCTAGGACTTAAACATATTCAAT 360
QY 372 GACAGGAAGATTTACACAGGAGCATAAAGCTCAGAACATTTTTCTTAGCAGAACCGGA 431
Db 361 GACAGGAAGATTTACACAGGAGCATAAAGCTCAGAACATTTTTCTTAGCAGAACCGGA 420
QY 432 ATGTTGGCAAGCTTGGGACTTTGGTATAGCAAGAGTCTCTGAAATAATTTCCATCGAACTT 491
Db 421 ATGTTGGCAAGCTTGGGACTTTGGTATAGCAAGAGTCTCTGAAATAATTTCCATCGAACTT 480
QY 492 GCTGGAATCTGATTTGNAACACCTTACTACCTGTCCCAGAGATCTGTCAGAAATAACCC 551
Db 481 GCTGGAATCTGATTTGNAACACCTTACTACCTGTCCCAGAGATCTGTCAGAAATAACCC 540
QY 552 TACAAATAAAGCGGATATTGGTCTCTTGGCTGTCTTATATAGCTCTGCACACTT 611
Db 541 TACAAATAAAGCGGATATTGGTCTCTTGGCTGTCTTATATAGCTCTGCACACTT 600
QY 612 AAACATCTTTTGGGTTAAACATTTACAGCAGCTGGTTCTGAAGATTTGTCAAGCAGCAT 671
Db 601 AAACATCTTTTGGGTTAAACATTTACAGCAGCTGGTTCTGAAGATTTGTCAAGCAGCAT 660
QY 672 TTTGCCCAATATCTCGGGGTTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 731
Db 661 TTTGCCCAATATCTCGGGGTTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 720
QY 732 CAAGTATCTCTCGAGACCGACCATCCATAAATTTCCATTTTGAAGGCCCTTTTAGAG 791
Db 721 CAAGTATCTCTCGAGACCGACCATCCATAAATTTCCATTTTGAAGGCCCTTTTAGAG 780
QY 792 AATCTTATTTCCAAATATTTGAGCTCTCAGGCTCAATCAGGAGAAATTCAGTCACATGCTT 851
Db 781 AATCTTATTTCCAAATATTTGAGCTCTCAGGCTCAATCAGGAGAAATTCAGTCACATGCTT 840

Matches 1215; Conservative 0; Mismatches 4; Indels 3; Gaps 1;			
QY	1	CATTGAGACCATGATAGTACGATGTGATTAAGCCATCGGCAAGTGCCTTCGGGA	60
Db	88	CATTGAGACCATGATAGTACGATGTGATTAAGCCATCGGCAAGTGCCTTCGGGA	147
QY	61	AAGCATATCTAGCTAAGGGAATCAGATAGCAAGCACTGTGTCTATAAAGAGATCAATT	120
Db	148	AAGCATATCTAGCTAAGGGAATCAGATAGCAAGCACTGTGTCTATAAAGAGATCAATT	207
QY	121	TTGAAAAGATGCCATACAGAAAAGAGAGCTTCAAGAAAAGAGTATCTTCTGGAAA	180
Db	208	TTGAAAAGATGCCATACAGAAAAGAGAGCTTCAAGAAAAGAGTATCTTCTGGAAA	267
QY	181	AGATGAAACATCCCAACATTTAGCTTCTCAATTCATTTCAAGAGAAATGCGAGCTGT	240
Db	268	AGATGAAACATCCCAACATTTAGCTTCTCAATTCATTTCAAGAGAAATGCGAGCTGT	327
QY	241	TTATTGTAATGGAATTTGTATGAGGGGATCTCATGAAAGGATCAATAGACAACGGG	300
Db	328	TTATTGTAATGGAATTTGTATGAGGGGATCTCATGAAAGGATCAATAGACAACGGG	387
QY	301	GTGTGTTATTAGTGAAGATCAGATCCTCGGTTGGTTGTACAGATTTCTTAGACTAA	360
Db	388	GTGTGTTATTAGTGAAGATCAGATCCTCGGTTGGTTGTACAGATTTCTTAGACTAA	447
QY	361	AACATATTCATGACAGGAAGATATTACAGGGACATAAAGCTCAGAACATTTTCTTA	420
Db	448	AACATATTCATGACAGGAAGATATTACAGGGACATAAAGCTCAGAACATTTTCTTA	507
QY	421	GCAAGACCGAATGGTGGCAAGCTTTGGGACCTTGGTATACAGAGCTCCTGAATATT	480
Db	508	GCAAGACCGAATGGTGGCAAGCTTTGGGACCTTGGTATACAGAGCTCCTGAATATT	567
QY	481	CCATGGAACCTTGCTCGAATCTGTATTGGAACACCTTACTACCTGCCAGAGATCTGTC	540
Db	568	CCATGGAACCTTGCTCGAATCTGTATTGGAACACCTTACTACCTGCCAGAGATCTGTC	627
QY	541	AGAATAAACCCATACACAATAAAGGATTTGGTCTCTTGGCTGTGCTTATATGAGC	600
Db	628	AGAATAAACCCATACACAATAAAGGATTTGGTCTCTTGGCTGTGCTTATATGAGC	687
QY	601	TCGTGCACATTAAACATCTTTGAGGTAACCACTTACAGACGCTGGTTCTTGAATTT	660
Db	688	TCGTGCACATTAAACATCTTTGAGGTAACCACTTACAGACGCTGGTTCTTGAATTT	747
QY	661	GTCAGCACATTTTGCCCAATATCTCCGGGGTTTTCTCGTGAGCTCCATTCCTTGAT	720
Db	748	GTCAGCACATTTTGCCCAATATCTCCGGGGTTTTCTCGTGAGCTCCATTCCTTGAT	807
QY	721	CTCAGCTCTTCAAGTATCTCCTCGAGACCGACCATCCATTAATTCATTTTGAAGGC	780
Db	808	CTCAGCTCTTCAAGTATCTCCTCGAGACCGACCATCCATTAATTCATTTTGAAGGC	867
QY	781	CTTTTGTAGAGATCTTATTTCCCAATATTGACTCTCTGAGGTCA---TTCAGGAAGAT	837
Db	868	CTTTTGTAGAGATCTTATTTCCCAATATTGACTCTCTGAGGTCA---TTCAGGAAGAT	927
QY	838	TCAGTCACATGCTTATATGACAGAGAGAGCGCCAGCTTCTCGACATGCTGGGAAGTGG	897
Db	928	TCAGTCACATGCTTATATGACAGAGAGAGCGCCAGCTTCTCGACATGCTGGGAAGTGG	987
QY	898	TCAGAGAGTGTAAAATACAAAAGAGTGAGATTCCGGGGAAAGTGCCCAACCAAGATCAAGA	957
Db	988	TCAGAGAGTGTAAAATACAAAAGAGTGAGATTCCGGGGAAAGTGCCCAACCAAGATCAAGA	1047
QY	958	TATCTGTGCCAATTAAGAAGATGCTATATTGATGAAATGAATGAGACCAACAGCTG	1017
Db	1048	TATCTGTGCCAATTAAGAAGATGCTATATTGATGAAATGAATGAGACCAACAGCTG	1107
QY	1018	GAGCCAGAGGCGCAGATCTATAAATGATAGAAAGCCCAAAATTCGTGCTGTG	1077
Db	1108	GAGCCAGAGGCGCAGATCTATAAATGATAGAAAGCCCAAAATTCGTGCTGTG	1167

RESULT 8	
US-10-114-270-185	
; Sequence 185, Application US/10114270	
; Publication No. US20040030110A1	
; GENERAL INFORMATION:	
; APPLICANT: Guo, Xiaojia	
; APPLICANT: Kekuda, Ramesh	
; APPLICANT: Miller, Charles E.	
; APPLICANT: Malyankar, Uriel M.	
; APPLICANT: Spytek, Kimberly A.	
; APPLICANT: Patturajan, Meera	
; APPLICANT: Liu, Ziaohong	
; APPLICANT: Gusev, Vladimir Y.	
; APPLICANT: Li, Li	
; APPLICANT: Vernet, Corine	
; APPLICANT: Zehusen, Bryan D.	
; APPLICANT: Gorman, Linda	
; APPLICANT: Shenoy, Suresh G.	
; APPLICANT: Pena, Carol E.A.	
; APPLICANT: Smithson, Glennda	
; APPLICANT: Burgess, Catherine E.	
; APPLICANT: Gerlach, Valerie	
; APPLICANT: Padigaru, Muralidhara	
; APPLICANT: Shinkets, Richard A.	
; APPLICANT: Gangolli, Esha A.	
; APPLICANT: Taupier Jr., Raymond J.	
; APPLICANT: Casman, Stacie J.	
; APPLICANT: Ji, Weizhen	
; APPLICANT: Anderson, David W.	
; APPLICANT: Liete, Mario W.	
; APPLICANT: Rastelli, Luca	
; APPLICANT: Edinger, Shlomit R.	
; APPLICANT: Stone, David J.	
; APPLICANT: MacDougall, John R.	
; APPLICANT: Rothenberg, Mark E.	
; TITLE OF INVENTION: No. US20040030110A1el Proteins and Nucleic Acids Encoding Same	
; FILE REFERENCE: 21402-322C	
; CURRENT APPLICATION NUMBER: US/10/114, 270	
; CURRENT FILING DATE: 2002-11-27	
; PRIOR APPLICATION NUMBER: 60/281, 086	
; PRIOR FILING DATE: 2001-04-03	
; PRIOR APPLICATION NUMBER: 60/281, 136	
; PRIOR FILING DATE: 2001-04-03	
; PRIOR APPLICATION NUMBER: 60/281, 863	
; PRIOR FILING DATE: 2001-04-05	
; PRIOR APPLICATION NUMBER: 60/281, 906	
; PRIOR FILING DATE: 2001-04-05	
; PRIOR APPLICATION NUMBER: 60/282, 020	
; PRIOR FILING DATE: 2001-04-06	
; PRIOR APPLICATION NUMBER: 60/282, 930	
; PRIOR FILING DATE: 2001-04-10	
; PRIOR APPLICATION NUMBER: 60/282, 934	
; PRIOR FILING DATE: 2001-04-10	
; PRIOR APPLICATION NUMBER: 60/283, 512	
; PRIOR FILING DATE: 2001-04-12	
; PRIOR APPLICATION NUMBER: 60/283, 710	
; PRIOR FILING DATE: 2001-04-13	
; PRIOR APPLICATION NUMBER: 60/284, 234	
; PRIOR FILING DATE: 2001-04-17	

QY	1078	GACATTATGATTATTATTATGCTCAACTTGATATGCTGAGGAGAGAGCCACAAACCAA	1137
Db	1168	GACATTATGATTATTATTATGCTCAACTTGATATGCTGAGGAGAGAGCCACAAACCAA	1227
QY	1138	GTTATCACCTTATTCCTCAAGAAATATCTGGAGTTGAGGATTAACGTCAGGAAACGAGGC	1197
Db	1228	GTTATCACCTTATTCCTCAAGAAATATCTGGAGTTGAGGATTAACGTCAGGAAACGAGGC	1287
QY	1198	ATGCTCCATCCCAAGTCAATG	1219
Db	1288	ATGCTCCATCCCAAGTCAATG	1309

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 470
; SEQ ID NO 185
; LENGTH: 1453
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1198)
US-10-114-270-185

Query Match 49.7%; Score 1176.8; DB 16; Length 1453;
Best Local Similarity 99.1%; Pred. No. 5.3e-302;
Matches 1197; Conservative 0; Mismatches 2; Indels 9; Gaps 1;

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QY 12 ATGGATAAGTACGATGTGATTAAAGCCATCGGGCAAGGTGCTTCGGGAAAGCATCTTA 71
Db 1 ATGGATAAGTACGATGTGATTAAAGCCATCGGGCAAGGTGCTTCGGGAAAGCATCTTA 60
QY 72 GCTAAGGGAATCAGATAGCAAGCACTGTCTCATAAAGAGATCAATTTTGAAGATG 131
Db 61 GCTAAGGGAATCAGATAGCAAGCACTGTCTCATAAAGAGATCAATTTTGAAG--- 117
QY 132 CCCATACAGAAAAAGAGCTTCAAAGAAAGAGTGAATTCCTCGGAAAGATGAACAT 191
Db 118 -----CAAGAAAAAGAGCTTCAAAGAAAGAGTGAATTCCTCGGAAAGATGAACAT 171
QY 192 CCCACATGTAGCCCTCTTCAATTCATTTCAAGAGATGCGAGCGTGTATTGTAATG 251
Db 172 CCCACATGTAGCCCTCTTCAATTCATTTCAAGAGATGCGAGCGTGTATTGTAATG 231
QY 252 GAATATTGTGATGGAGGGATCTCATGAAAAAGGATCAATACAAACGGGTGTCTATT 311
Db 232 GAATATTGTGATGGAGGGATCTCATGAAAAAGGATCAATACAAACGGGTGTCTATT 291
QY 312 AGTGAAGATCAGATCCTCGGTGGTGTGTAAGATTTCTTAGACCTAAACATATTTCAT 371
Db 292 AGTGAAGATCAGATCCTCGGTGGTGTGTAAGATTTCTTAGACCTAAACATATTTCAT 351
QY 372 GACAGGAAGATATTACAGAGGACATAAAGCTCAGAACATTTTCTTAGCAAGACGGA 431
Db 352 GACAGGAAGATATTACAGAGGACATAAAGCTCAGAACATTTTCTTAGCAAGACGGA 411
QY 432 ATGTGGCAAGCTTGGGACTTTGGTATAGCAAGAGTCTCTGAATAATTCCATGGAACT 491
Db 412 ATGTGGCAAGCTTGGGACTTTGGTATAGCAAGAGTCTCTGAATAATTCCATGGAACT 471
QY 492 GCTCGAATCTGATTGGACACCTTACTACCTGTCCCAGAGATCTCTCAGATAAACCC 551
Db 472 GCTCGAATCTGATTGGACACCTTACTACCTGTCCCAGAGATCTCTCAGATAAACCC 531
QY 552 TACAACTAAAGCGATATTGGTCTCTTGGCTGTCTTATATAGCTCTGCACACTT 611
Db 532 TACAACTAAAGCGATATTGGTCTCTTGGCTGTCTTATATAGCTCTGCACACTT 591
QY 612 AAACATCTTTTGGGGTAAACACTTACAGAGCTGGTGTGAAGATTGTCAAGCAT 671
Db 592 AAACATCTTTTGGGGTAAACACTTACAGAGCTGGTGTGAAGATTGTCAAGCAT 651
QY 672 TTTGCCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCTTGTATATCTCAGCTCTT 731
Db 652 TTTGCCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCTTGTATATCTCAGCTCTT 711
QY 732 CAAGTATCTCTCGAGACCGACCAATCCATAAATTCATTTTGAAGAGCCCTTTTAGAG 791
Db 712 CAAGTATCTCTCGAGACCGACCAATCCATAAATTCATTTTGAAGAGCCCTTTTAGAG 771
QY 792 AATCTTATTTCCCAATATTTCAGCTCCCTGAGGTCAATTCAGGAAGATTCAGTCACTGCT 851
Db 772 AATCTTATTTCCCAATATTTCAGCTCCCTGAGGTCAATTCAGGAAGATTCAGTCACTGCT 831
QY 852 ATATGCAAGAGGAGCGCCAGCTTCTCGACATCTCGGAGGTGGTCCAGAGGTGTA 911
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Db 832 ATATGCAAGAGGAGCGCCAGCTTCTCGACATGTGTGGAAAGGTGGTCCAGAGGTGTA 891
QY 912 ATACAAAAAGTGGATTCGGGGAAAGTCCCAACCAAGATCAAGGATATCTCTGCAATT 971
Db 892 ATACAAAAAGTGGATTCAGGGAAAGTCCCAACCAAGATCAAGGATATCTCTGCAATT 951
QY 972 AAAAGGAATGCTATATTGTCATAGAAATGAATGAGACCAACCAAGCTGGAGCCAGAGGCC 1031
Db 952 AAAAGGAATGCTATATTGTCATAGAAATGAATGAGACCAACCAAGCTGGAGCCAGAGGCC 1011
QY 1032 AGATCTATAAAATGATAGAAAGACCCAAAATTTGCTGTCTGTGTGGACATTTATGATTAT 1091
Db 1012 AGATCTATAAAATGATAGAAAGACCCAAAATTTGCTGTCTGTGTGGACATTTATGATTAT 1071
QY 1092 TATTATGCTCAACTGTTGATATGCTGAGGAGGAGGCCCAACCAAGTTATCCCTATT 1151
Db 1072 TATTATGCTCAACTGTTGATATGCTGAGGAGGAGGCCCAACCAAGTTATCCCTATT 1131
QY 1152 CCTCAAGAAATACCTGGAGTTTGGAGTTACGGTCAAGGAAACGAGCATGTTCCATCCCA 1211
Db 1132 CCTCAAGAAATACCTGGAGTTTGGAGTTACGGTCAAGGAAACGAGCATGTTCCATCCCA 1191
QY 1212 AGTCAATG 1219
Db 1192 AGTCAATG 1199
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RESULT 9

US-09-783-320-50
; Sequence 50, Application US/09783320
; Patent No. US20020038011A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Turner, C. Alexander Jr
; APPLICANT: Zambrowicz, Brian
; TITLE OF INVENTION: NO. US20020038011A1el Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0137-USA
; CURRENT APPLICATION NUMBER: US/09/783,320
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: US 60/183,582
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/184,014
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 5426
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-783-320-50

Query Match 15.6%; Score 369.4; DB 9; Length 5426;
Best Local Similarity 66.0%; Pred. No. 8e-87;
Matches 551; Conservative 0; Mismatches 281; Indels 3; Gaps 1;

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QY 9 ACCATGGGTAAGTACGATGTGATTAAAGGCCATCGGGCAAGGTGCTTCGGGAAAGCATAC 68
Db 531 ATCATGGAGAGTATGTTAGACTACAGAAAGATTGGAGAAGGTTCATTGGAAGGCCATT 590
QY 69 TTAGCTAAGGGAATCAGATAGCAGCACTGTGTCTATAAAGAGATCAATTTTGAAG 128
Db 591 CTTGTTAAATCTACAGAAAGATGGCAGACAGTATGTTATCAAGGAAATTAACATCTCAGA 650
QY 129 ATGCCCATACAGAAAAAGAGCTTCAAGAAAAAGAGTGAATTTCTTGGAAAAAGATGAAA 188
Db 651 ATGTCCAGTAAGAAGAGAGAGATCAAGGAGAGAGTTGCAAGTATGGCAACATGAG 710
QY 189 CATCCCAACATGTAGCCCTTCTCAATTCATTTCAAGAGATGCGAGCTGTTTATTGTA 248
Db 711 CATCCAAATATTGTCCAGTATAGAGAAATCAATTTGAAGAAATGGCTCTCTCTACATAGTA 770
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249 ATGGAATATTGTGATGGAGGGATCTCATCAAAGGATCAATAGACAACGGGTGTGTTA 308
771 ATGCATTACTGTGAGGGAGGGATCTGTTTAAGCGAATAAATGCTCAGAAAGGCGTTTG 830
309 TTTAGTGAAGATCAGATCCTCGTGTGTTTGTACAGATTTCTTAGGACTAAACATATT 368
831 TTTCAAGAGATCAGATTTTGGACTGTTTGTACAGATATGTTGGCCCTGAAACATGTA 890
369 CATGACAGGAAGATATTACACAGGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAAC 428
891 CATGATAGAAAATTTCTCATCGAGACATTAATCTCAGAACATATTTTAATAAGAT 950
429 GGAATGGTGCAGAAAGCTTGGGACTTGTGTATAGCAAGAGTCTGTAATATTCATGGA 488
951 GGAACAGT---ACAACCTTGGAGATTTTGGAAATTTGCTAGAGTTCTTAATAGTACTGTAG 1007
489 CTTCCTCGAATTTGTAATGGAACACCTTACTCTCTCCAGAGATCTGTGAGATAAA 548
1008 CTGCTCGAATTTGCAATAGGACCCCATCTACTTGTACCTGAAATCTGTGAAACAAA 1067
549 CCTACAAACAATAAAACGGATATTGCTCTTGGCTGTGTCTTATATGAGCTCTGCACA 608
1068 CCTTACAATAATAAAAGTGACATTTGGGCTCTGGGCTGTGCTCTTATGAGCTGTGACA 1127
609 CTTAATACATCTTTGAGGGTAAACACTTACAGCAGCTGGTCTGAGAGATTTGTCAAGCA 668
1128 CTTAAACATGCTTTTGAAGCTGGCAGTATGAAAAAACCCTGCTACCTGAAATCTGTGAAAACAAA 1307
789 GAGAACTTATTCCTCCAAATATTGAGTCTCTGAGGTCTTCTGAGTCTTCTGAGTCTCAGCTC 843
1308 GCCAAACGCATTGAAAAGTTTCTCTCTCTCAGCTTATTGCAAGAGATTTTGTGTC 1362

RESULT 10

US-10-037-270-246
; Sequence 246, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyun
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aigong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunding
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Tillinghast, John
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/10/037,270
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104

; SOFTWARE: pt FL_genes Version 1.0
; SEQ ID NO 246
; LENGTH: 5448
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (534)..(4178)
US-10-037-270-246

Query Match 15.6%; Score 369.4; DB 15; Length 5448;
Best Local Similarity 66.0%; Pred. No. 8e-87;
Matches 551; Conservative 0; Mismatches 281; Indels 3; Gaps 1;
QY 9 ACCATGATAGTACGATGTGATTAAAGCCCATCGGCAAGTGTCTTCGGGAAAGCATAC 68
Db 531 ATCATGAGAGATGTTAGACATACAGAGATTGGAGAGGTTCAITTTGAAAAGCCATT 590
QY 69 TTAGCTAAAGGAAATCAGATAGCAAGCACTGTGTCTATAAAGAGATCAATTTTGAAGA 128
Db 591 CTTGTTAAATCTACAGAAAGATGGCAGACAGTATGTTTATCAAGGAAATTAACATCTCA 650
QY 129 ATGCCCATACAGAAAAGAGCTTCAAGAAAAGAGTGTCTTCTGGAAGAGATCAAA 188
Db 651 ATGTCCAGTAAGAAAGAGAGAGATCAAGGAGAGAGTTCAGTATTGGCAACATGAG 710
QY 189 CATCCCAACATTTAGGCTTTCTCAATTCATTTCAAGAGATGGCAGGCTGTTTATTGTA 248
Db 711 CATCCAAATATTGCCAGTATAGAGAAATCAATTTGAAGAAAATGGCTCTCTACATAGTA 770
QY 249 ATGGAATATTGTGATGAGGGGATCTCATGAAAGGATCAATAGACAACGGGTGTGTTA 308
Db 771 ATGGAATTACTGTGAGGAGGGGATCTGTTTAAAGCAATAAATGCTCAGAAAGGCTTTTG 830
QY 309 TTTAGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTTCTTAGGACTAAAACATATT 368
Db 831 TTTCAAGAGGATCAGATTTTGGACTGTTTGTACAGATATGTTTGGCCCTGAAACATGTA 890
QY 369 CATCAGAGAGATATTACACAGGACATAAAGCTCAGAACATTTTCTTAGCAAGAAC 428
Db 891 CATGATAGAAAATTTCTTCATCGAGACATTAATTTCTCAGAACATATTTTAACTAAAGAT 950
QY 429 GGAATGGTGGCAAAAGCTTGGGACTTTGGTATAGCAAGAGTCTCTGAATAATTTCCATGAA 488
Db 951 GGAACAGT---ACAACCTTGGAGATTTTGGAAATTTGCTAGAGTTCTTAATAGTACTGTAG 1007
QY 489 CTTCCTCGAATTTGTATTTGAAACACCTTACTACTGTCCCAAGAGATCTGTCAAGATAAA 548
Db 1008 CTGGCTCGAATTTGCATAGGGACCCCATACTACTTGTCACTGAAATCTGTGAAAACAAA 1067
QY 549 CCCTACACAAATAAAACGGATATTGCTCTCTGGCTGTGCTTATATGAGCTCTGCACA 608
Db 1068 CTTTACAATAATAAAGTGACATTTGGGCTCTGGGTTGTCTCTTTATGAGTGTGTACA 1127
QY 609 CTTAAACATCCTTTTGGAGGTAAACACTTACAGCAGCTGGTTCTGAGAGATTTGTCAAGCA 668
Db 1128 CTTAAACATGCTTTTGAAGCTGGCAGTATGAAAAAACCCTGCTACCTGAAAGATAATATCTGA 1187
QY 669 CATTTTGGCCCAATATCTCGGGGTTTCTCGTGTGAGTCCATCTCTGATATCTCAGCTC 728
Db 1188 TCCTTTCCACCTGTGCTTTTGCATATTCTCTATGATCTCCGAGTTTGGGTCTCAGTTA 1247
QY 729 TTTCAAGTATCTCTCGAGACCCGACCATCTCTGAGCTCCATCTCTTGATATCTCAGCTC 788
Db 1248 CTTAAAGAAATCTTGAAGCTGGCAGTATGAAAAAACCCTGCTACCTGAAAGATTTTGTGTC 1307

RESULT 11

US-10-117-722-246

```
; Sequence 246, Application US/1011722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030219744A1el Nucleic Acids and
; FILE REFERENCE: 784CIP2BGP
; CURRENT APPLICATION NUMBER: US/10/117,722
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 246
; LENGTH: 5448
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (534)..(4178)
US-10-117-722-246

Query Match          15.6%; Score 369.4; DB 15; Length 5448;
Best Local Similarity 66.0%; Pred. No. 8e-87;
Matches 551; Conservative 0; Mismatches 281; Indels 3; Gaps 1;

QY 9 ACCATGGTAAGTACGATGTCATTAAGGCCCATCGGCAAGGTGCTTCGGAAAGCATAC 68
DB 1128 CTTAAACATGCTTTTGAAGCTGGCAGATGATGAAGAACCTGGTACTGAAGATAATATCTGGA 1187
QY 669 CATTTTGGCCCAATATCTCCGGGGTTTTCTCGTAGCTCCATTCCTTGTATCTCAGCTC 728
DB 1188 TCTTTTCCACCTGTCTCTTTCGATTAATTCCTATGATCTCCGAGTTTGGTGTCTCAGTTA 1247
QY 729 TTTCAAGTATCTCTCGAGACCGACCATCCATAAAATTCATTTTGAAAAGGCCCTTTTATA 788
DB 1248 TTTAAAGAAATCTTAGGATAGACCAATCAGTCAATCTCAATTTGGAGAAAGTTTATA 1307
QY 789 GAGATCTTATTTCCCAATATTTGATCTCTGAGGTCAATTCAGGAAGAAATTCAGTC 843
DB 1308 GCCAAACGCAATGAAAGTTTCTCTCTCTCAGCTTATTGCAAGAAATTTTGTG 1362

RESULT 12
US-10-037-270-245
; Sequence 245, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Tillinghast, John
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/10/037,270
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 245
; LENGTH: 5532
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (534)..(4262)
US-10-037-270-245

Query Match          15.6%; Score 369.4; DB 15; Length 5532;
Best Local Similarity 66.0%; Pred. No. 8.1e-87;
Matches 551; Conservative 0; Mismatches 281; Indels 3; Gaps 1;

QY 9 ACCATGGTAAGTACGATGTCATTAAGGCCCATCGGCAAGGTGCTTCGGAAAGCATAC 68
DB 531 ATCATGGAGAAGTATGTTAGACTACAGAAGATTGGAGAAGGTTCATTTGGAAAGCCATT 590
QY 69 TTAGCTAAAGGAATCATAGTAGACGACCTGTGTCTATAAAGAGATCAATTTTGAAG 128
DB 591 CTTGTAAATCTACAGAAGATGGCAGACAGATGTGTATCAAGGAATTAACATCTCAAGA 650
QY 129 ATGCCCATACAGAAAGAGCTTCAAAGAAAGAGTGAATCTTCTCGAAAAGATGAAA 188
DB 651 ATGTCACGTAAAGAAAGAGAGATCAAGGAGAGAGTTGCAGTATTGGCAACATCAAG 710
QY 189 CATCCCAATCTGAGCTTCTCAATTCATTTCAAGAGATGCGAGGCTGTTTATTGTA 248
DB 711 CATCCAAATATTGTCCAGTATAGAGAATCAATTTGAAGAAATGGCTCTCTCTACATAGTA 770
QY 249 ATGGAATATTGTGAGGAGGGATCTCATGAAAGAGTCAATAGACAACGGGGTGTGTTA 308
DB 771 ATGGATTACTGTGAGGAGGGGATCTGTTTAAGCGAATAATGCTCAGAAGGGGTTTG 830
QY 309 TTTAGTGAAGATCAGATCCTCGTGTGTTGTTGTAAGATTTCTTAGACTATAAACAATTT 368
DB 831 TTTCAAGAGATCAGATTTTGGACTGTTGTACAGATATGTTTGGCCCTGAAACAATGTA 890
QY 369 CATGACAGGAAGATATTACAGGGACATAAAGCTCAGAACATTTTCTTAGCAAGAAC 428
DB 891 CATGATAGAAATTTCTTCATCGAGACATTAATCTCAGAACATATTTTAACTAAGAT 950
QY 429 GGAATGTTGGCAAGCTTTGGGACTTTGGTATAGCAAGAGTCTCGAATAATTTCAATGAA 488
DB 951 GGAACAGT---ACAACITGGAGATTTTGAATTTGAGATTTCTTAATAGTACTGTAGAG 1007
QY 489 CTTGCTCGAAGCTGTATTGGACACCTTACTACCTGTCGCCAGAGATCTCTCAGATAAA 548
DB 1008 CTGGCTCGAAGCTGTATAGGACCCCTACTACTTGTACCTGTAATCTGTGAAACAAA 1067
QY 549 CCCTACAAACAATAAACGGATATTGTTGCTCTCTGCTGTGTCTTATATGAGCTCTGCACA 608
DB 1068 CTTTACAAATAAAGAGTACATTTGGGCTCTGGGGTGTGCTCTTATGAGTGTGTGACA 1127
```



```
Db 651 ATGTCCAGTAAAGAAAGAGAAATCAAGGAGAGAAAGTTGCAGTATTGGCAACATGAAG 710
Qy 189 CATCCCAACATTGTAGCCTCTTCAATTCAATTTCAAGAGAAATGCGAGGCTGTTTATTGTA 248
Db 711 CATCCAAATATTGTCAGATATAGAGATCATTTGAAGAAATGGCTCTCTACATAGTA 770
Qy 249 ATGGAATATTGTGATGAGGGGATCTCATGAAAGAGATCAATAGACAACGGGTGTGTTA 308
Db 771 ATGGAATTACTGTGAGGGAGGGATCTGTTTAAGCGAATAAATGCTCAGAAAGCGGTTTG 830
Qy 309 TTTAGTGAAGATCAGATCCTCGGTGTTTGTACAGATTTCTAGGATTAACATATT 368
Db 831 TTTCAAGAGATCAGATTTGGACTGTTTGTACAGATATTGTTGCCCTGAAACAATGA 890
Qy 369 CATGACAGGAGATATTACACAGGACATAAAAGCTCAGAACATTTTTTCTTACAGAAAC 428
Db 891 CATGATAGAAAATTTCTTCATCGAGACATTAATCTCAGAACATATTTTAACTAAGAT 950
Qy 429 GGAATGGTGCAAGCTTGGGACTTTGGTATAGCAAGAGTCTGTAATTAATTCATGGA 488
Db 951 GGAACAGT---ACAACCTGGAGATTTTGGAAATTGCTAGAGTTCTTAATAGTACTGTAG 1007
Qy 489 CTGTGCTCGAACTTGTATTGGAACACCTTACTACTGCTCCACAGATCTGTCAAGATAAA 548
Db 1008 CTGGCTCGAACTTGCATAGGACCCCATACTACTTGTCACTGAAATCTGTGAACAAA 1067
Qy 549 CCTACAAACATAAAACGGATATTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 608
Db 1068 CTTTACAAATAAATAAAGTGACATTTGGGCTCTGGGCTGCTGCTGCTGCTGCTGCTGCTG 1127
Qy 609 CTTTAAACATCCTTTTGGAGGTAAACATTAACAGCAGCTGCTGCTGCTGCTGCTGCTGCT 668
Db 1128 CTTTAAACATCCTTTTGGAGGTAAACATTAACAGCAGCTGCTGCTGCTGCTGCTGCTGCT 1187
Qy 669 CATTTTGGCCCAATATCTCGGGGTTTCTCTGAGCTCCATTCCTTGATATCTCAGCTC 728
Db 1188 TCCTTTCCACCTGTGCTTTGCAATTAATTCCTATGATCTCGGAGTTTGGTGTCTCAGTTA 1247
Qy 729 TTTCAAGTATCTCTCGAGACCCGACCATCCATAAATTCATTTTGAAGGCCCTTTTATA 788
Db 1248 TTTAAAGAAATCCTAGGATAGACCATCAGTCAACTCCCATATTGAGAAAGGTTTATA 1307
Qy 789 GAGAATCTTATTTCCCAATATTGACCTCCTGAGCTCCATTCAGGAGAAATTCAGTC 843
Db 1308 GCCAAACGCATTGAAAGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1362
```

RESULT 13

```
US-10-117-722-245
; Sequence 245, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP25CIP
; CURRENT APPLICATION NUMBER: US/10/117,722
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 245
; LENGTH: 5532
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (534)..(4262)
US-10-117-722-245
```

Query Match 15.6%; Score 369.4; DB 15; Length 5532;
Best Local Similarity 66.0%; Pred. No. 8.1e-87;

Mismatches 551; Conservative 0; Mismatches 281; Indels 3; Gaps 1;

```
Qy 9 ACCATGGATAGTACGATGTGATTAAGCCATCGGCAAGGTGCTTCGGGAAAGCATAC 68
Db 531 ATCATGGAGAGTATGTTAGACTACAGAAGATTGGAGAAGGTTTCATTGGGAAAGCCATT 590
Qy 69 TTAGCTAAAGGGAATCAGATAGCAAGCACCTGTCTCAATAAAGAGATCAATTTTGAAGA 128
Db 591 CTGTGTAAATCTACAGAAGATGGCAGACAGTATGTTATCAAGGAAATTAATCTCAGA 650
Qy 129 ATGCCCATACAGAAAAAGAGCTTTCAAGAAAGAGTATCTTCTGGAAAAAGATGAAA 188
Db 651 ATGTCAGTAAGAAAGAGAAAGAAATCAAGGAGAGAAAGTTGCAGTATTGGCAACATGA 710
Qy 189 CATCCCAACATTGTAGCCTTCTTCAATTTCAATTTCAAGAGATGCGAGCTCTGTTATTGTA 248
Db 711 CATCAAAATATTGCCAGTATAGAGATCATTTGAAGAAATGGCTCTCTCTCATAGTA 770
Qy 249 ATGGAATATTGTGATGGAGGGATCTCATGAAAAAGGATCAATAGACAACGGGGTGTGTTA 308
Db 771 ATGGATTAATCTGAGGGAGGGGATCTGTTTAAAGCGAATAAATGCTCAGAAAGGCGTTTG 830
Qy 309 TTTAGTGAAGATCAGATCCTCGGTGTTTGTAGAGATTTCTTAGGACTTAAACATATT 368
Db 831 TTTCAAGAGGATCAGATTTTGGACTGTTTGTACAGATATGTTTGGGCTTGAACATGTA 890
Qy 369 CATGACAGAAAGATATTACACAGGAGATAAAGAGCTCAGAACATTTTCTTAGCAAGAAC 428
Db 891 CATGATAGAAAATTTCTTCATCGAGACATTAATTCCTCAGAACATTTTAACTAAAGAT 950
Qy 429 GGAATGGTGGCAAGCTTGGGAGCTTTGGTATAGCAAGAGTCTGTAATTAATTCATGGA 488
Db 951 GGAACAGT---ACAACCTGGAGATTTTGGAAATTGCTAGAGTTCTTAATAGTACTGTAG 1007
Qy 489 CTGTGCTCGAACTTGTATTGGAACACCTTACTACTGCTCCACAGATCTGTCAAGATAAA 548
Db 1008 CTGGCTCGAACTTGCATAGGACCCCATACTACTTGTCACTGAAATCTGTGAACAAA 1067
Qy 549 CCCTACAAACATAAAAACGGATATTGTTGCTCTCTGAGCTCCATTCCTTGATATGAGCTCTG 608
Db 1068 CCTTACAAATAAATAAAGTGACATTTGGGCTCTGGGCTGCTGCTTATGAGCTGTGACA 1127
Qy 609 CTTTAAACATCCTTTTGGAGGTAAACATTAACAGCAGCTGCTGCTGCTGCTGCTGCTGCT 668
Db 1128 CTTTAAACATGCTTTTGAAGCTGGCAGTATGAAACCTGGTACTGGAAGATAATATCTGGA 1187
Qy 669 CATTTTGGCCCAATATCTCGGGGTTTCTCTGAGCTCCATTCAGTATCTCAGCTC 728
Db 1188 TCCTTTCCACCTGTGCTTTGCAATTAATTCCTATGATCTCGGAGTTTGGTGTCTCAGTTA 1247
Qy 729 TTTCAAGTATCTCTCGAGACCCGACCATCCATAAATTCATTTTGAAGGCCCTTTTATA 788
Db 1248 TTTAAAGAAATCCTAGGATAGACCATCAGTCAACTCCCATATTGAGAAAGGTTTATA 1307
Qy 789 GAGAATCTTATTTCCCAATATTGACCTCCTGAGCTCCATTCAGGAGAAATTCAGTC 843
Db 1308 GCCAAACGCATTGAAAGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1362
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RESULT 14

```
US-10-618-941-29
; Sequence 29, Application US/10618941
; Publication No. US20040197792A1
; GENERAL INFORMATION:
```

APPLICANT: WHYTE, DAVID
APPLICANT: MANNING, GERARD
APPLICANT: CAENEPEEL, SEAN
TITLE OF INVENTION: NOVEL KINASES
FILE REFERENCE: 034536-0321
CURRENT APPLICATION NUMBER: US/10/618,941
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/395,632
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 143
SOFTWARE: PatentIn version 3.2
SEQ ID NO 29
LENGTH: 5583
TYPE: DNA
ORGANISM: Homo sapiens
US-10-618-941-29

Query Match 15.6%; Score 369.4; DB 18; Length 5583;
Best Local Similarity 66.0%; Pred. No. 8.1e-87; Mismatches 281; Indels 3; Gaps 1;
Matches 551; Conservative 0;

QY 9 ACCATGGATAAGTACCATGTGATTAAGGCCCATCGGCAAGGTGCTTCGGGAAAGCATAC 68
DB |||||
QY 490 ATCATGGAGAGTAGTGTAGACTACAGAAGATTGGAGAAGTTCATTGGAAAGCCATT 549
DB |||||
QY 69 TTAGCTAAAGGGAATCATAGATAGCAGCAGTGTGTATATAAGAGATCAATTTGAAAG 128
DB |||||
QY 550 CTGTGTAATCTACAGAAGATGGCAGACAGTATGTATCAAGGAAATTAACATCTCAAG 609
DB |||||
QY 129 ATGCCCATACAGAAAGAAAGAGCTTCAAGAAAGAAAGTGTCTCTGGAAGATGAAA 188
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QY 610 ATGTCAGTAAAGAAAGAAAGAAATCAAGGAGAGAGTTCAGTATTTGGCAACATGAG 669
DB |||||
QY 189 CATCCCAACATGTAGCCCTCTTCAATTCATTTCAAGAGAAATGCGAGCTGTTTATTGTA 248
DB |||||
QY 670 CATCCAAATATGTCCAGTATAGAGAAATCAATTTGAAGAAATGCTCTCTACATAGTA 729
DB |||||
QY 249 ATGGATATTTGATGGAGGGGATCTCATGAAGAGATCATACAGACGGGGTGCTTA 308
DB |||||
QY 730 ATGGATTTACTGTAGGGAGGGGATCTGTTTAAGCGAATAAATGCTCAGAAAGCGCTTTG 789
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QY 309 TTTAGTGAAGATCAGATCTCGTGTGTTGTACAGATTTCTTAGGACTAAACATATT 368
DB |||||
QY 750 TTTCAAGAGGATCAGATTTTGGACTGTTGTACAGATATGTTTGGCCCTGAAACATGTA 849
DB |||||
QY 369 CATGACAGAGATATTACAGGACATAAAGCTCAGACATTTTCTTAGCATAAACATATT 428
DB |||||
QY 850 CATGATAGAAAATTCCTCATCGAGACATTAATCTCAGAACATATTTTAACTAAGAT 909
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QY 489 CTGTCTGAACTGTATTGGAACACCTTACTACCTGTCCCGAGAGATCTGTGAGAAATAA 548
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QY 967 CTGGCTGAACTGTGATAGGAGCCCATACTACTTGTCACTGAAATCTGTGAAACAAA 1026
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QY 609 CTTAAACATCCTTTTGGAGGTAAACATTAACAGAGCTGGTTCTGAAGATTTGTCAAGCA 668
DB |||||
QY 1087 CTTAAACATGCTTTTGAAGCTGGCAGTATGAAAAACCTGGTACTGAAGATAATATCTGGA 1146
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QY 1147 TCTTTTCCACCTGTGCTTTTGTCAATTTCTTATGATCTCCCGAGTTTGGTGTCTCAGTTA 1206
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QY 729 TTTCAAGTATCTCTCGAGACCGACCATCCATAAATTCATTTTGAAGGCCCTTTTATA 788
DB |||||
QY 1207 TTTAAAGAAATCTCTAGGATAGACCATCAGTCAACTCCATATTGGAGAAAGGTTTATA 1266
DB |||||

QY 789 GAGAACTTTATTCCCAATATTGACTCTCTGAGGTCTATTCAGGAGAAATTCAGTC 843
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QY 1267 GCCAAACGCATTGAAAGAGTTTCTCTCTCTCCTCAGCTTATTGAGAGAAATTTGTC 1321
DB |||||

RESULT 15
US-09-783-320-3
Sequence 3, Application US/09783320
Patent No. US20020038011A1
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Hu, Yi
APPLICANT: Nepomnichy, Boris
APPLICANT: Turner, C. Alexander Jr
APPLICANT: Zambrowicz, Brian
TITLE OF INVENTION: NO. US20020038011A1 Human Kinases and Polynucleotides Encoding
FILE REFERENCE: LEX-0137-USA
CURRENT APPLICATION NUMBER: US/09/783,320
CURRENT FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: US 60/183,582
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: US 60/184,014
PRIOR FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 3645
TYPE: DNA
ORGANISM: homo sapiens
US-09-783-320-3

Query Match 15.5%; Score 368; DB 9; Length 3645;
Best Local Similarity 66.0%; Pred. No. 1.5e-86;
Matches 549; Conservative 0; Mismatches 280; Indels 3; Gaps 1;

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DB |||||
QY 72 GCTAAAGGAATCATAGTAGCAAGCACTGTCTCATAAAGAGATCAATTTTGAAAGATG 131
DB |||||
QY 61 GTTAAATCTACAGAAGATGCGCAGACAGTATGTTATCAAGGAAATTAACATCTCAAGATG 120
DB |||||
QY 132 CCATACAGAAAAAGAAAGCTTCAAGAAAGAAAGTGTCTTCTGAAAAAGATGAACAT 191
DB |||||
QY 121 TCCAGTAAAGAAAGAGAGAATCAAGGAGAGAAGTTGCAGTATTGGCAACATGAAGCAT 180
DB |||||
QY 192 CCCAATTTGTAGCCCTTCTCAATTCATTTCAAGAGATGGCAGGCTGTTTATTGTAATG 251
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QY 181 CCAATATTTGTCAGTATAGAGAATCATTTGAAGAAATGGCTCTCTCTACATAGTAATG 240
DB |||||
QY 252 GAATATTTGTAGTGGAGGGATCTCATGAAAGAGATCAATAGACAACGGGGTGTGTTATT 311
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DB |||||
QY 312 AGTGAAGATCAGATCCTCGTGGTGTGTTGTACAGATTTCTTAGAGCTAAACATATTGAT 371
DB |||||
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DB |||||
QY 372 GACAGGAAGATATTACAGAGGACATAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 431
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QY 492 GCTCGAAGCTGTATTGGAACACCTTACTACCTGTCGCCAGAGATCTGTCAGATAAACC 551
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QY 478 GCTCGAAGCTGTATGGGACCCCATCTACTGTCACTGAAATCTGTGAAAAAACAACCT 537
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DB |||||

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Db      658  TTCCACCTGTGTCTTTGCAATTATCTATGATCTCGGAGTTTGGTGTCTCAGTTATTT 717
Qy      732  CRAGTATCTCTCGAGACCGACCATCCATAAATTCATTTTGAAGGCCCTTTTAGAG 791
Db      718  AAAAGAAATCCTAGGATAGACCATCAGTCACTCCATATTGGAGAAAGTTTATAGCC 777
Qy      792  AATCTTATTCCTCCAAATATTGACTCCTGAGGTCAATTCAGGAAGAAATTCAGTC 843
Db      778  AAACGATTGAAAAGTTTCTCTCTCTCAGCTTATTGCAGAGAAATTTGTC 829

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 Job time : 4632 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2004, 21:12:58 ; Search time 6658 Seconds
(without alignments)
12971.187 Million cell updates/sec

Title: US-10-730-010-1

Perfect score: 2370

Sequence: 1 cattggagaccatgataag.....ctgtcatgccttaccagcg 2370

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1: *
2: gb_est2: *
3: gb_his: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1218.4	51.4	1483	CR598570	full-length
2	842.2	35.5	890	CR598570	full-length
3	825.6	34.8	980	CR598570	full-length
4	597.4	25.2	1434	CR598570	full-length
5	597.4	25.2	2407	CR598570	full-length
6	594	25.1	603	CR598570	full-length
7	574.8	24.3	872	CR598570	full-length
8	547.8	23.1	670	CR598570	full-length
9	516.8	21.8	928	CR598570	full-length
10	485	20.5	856	CR598570	full-length
11	464.8	19.6	603	CR598570	full-length
12	455.4	19.2	603	CR598570	full-length
13	442.4	19.1	659	CR598570	full-length
14	446.2	18.8	678	CR598570	full-length
15	392	16.5	639	CR598570	full-length
16	391.6	16.5	643	CR598570	full-length
17	369.4	15.6	1628	CR598570	full-length
18	364.6	15.4	857	CR598570	full-length
19	355.8	15.0	2070	CR598570	full-length
20	355.8	15.0	3568	CR598570	full-length
21	354.2	14.9	3568	CR598570	full-length
22	347	14.6	3103	CR598570	full-length
23	329.8	13.9	648	CR598570	full-length
24	320.2	13.5	904	CR598570	full-length

25	313.4	13.2	732	7	CN531454
26	309.6	13.1	706	6	CD802687
27	308	13.0	630	4	BJ029013
28	293.8	12.4	718	6	CB312741
29	274.2	11.6	700	7	CF531621
30	265.2	11.2	2465	3	AK045202
31	259.4	10.9	763	7	CN160628
32	258.4	10.9	498	5	EX342706
33	254.4	10.7	649	6	CD291255
34	248.8	10.5	860	5	BP142906
35	248.2	10.5	812	5	BU322582
36	244.2	10.3	913	5	EQ432111
37	242.4	10.2	908	5	EX375816
38	241.2	10.2	927	5	EU516066
39	241	10.2	907	6	CA790699
40	240.6	10.2	730	7	CN531024
41	239	10.1	1971	3	CR612915
42	238.8	10.1	819	6	CF285034
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ALIGNMENTS

RESULT 1
CR598570
LOCUS
DEFINITION full-length cDNA clone CSODL005YK18 of B cells (Ramos cell line)
1483 bp mRNA linear HTC 21-JUL-2004
Cot 25-normalized of Homo sapiens (human).

ACCESSION CR598570
VERSION CR598570.1 GI:50479377
KEYWORDS HTC; CNSLT_CDNA

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/

REFERENCE
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequençage : BP 191 91006 EVRY cedex - FRANCE (E-mail: segref@genoscope.cns.fr)

COMMENT
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODL005YK18"
/tissue_type="B cells (Ramos cell line)"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 51.4%; Score 1218.4; DB 3; Length 1483;
Best Local Similarity 99.9%; Pred. No. 5e-294;
Matches 1219; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Bj061491 BJ061491
83 CATTGGAGACCATGTAAGTACGATGTGATTAAAGCCATCGGCGGAGGTGCCTTCGGGA 142

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QY 61 AAGCATACTTAGCTAAAGGGAATCAGATAGCAGCACTGTGTCATATAAAGAGATCAATT 120
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QY 121 TTGAAAAGATGCCATACAGAAAAGAGAGCTTCAAAAGAAAAGAGTGAATCTTCTCGAAA 180
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DB 263 AGATGAACATCCCAACATTTGTAGCCTTCTTCAATTTCAAGAGATGGCAGCTGT 322
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DB 383 GTGTGTTATTTAGTGAAGATCAGATCCTCGGTGGTTGTTGTACAGATTTCTTAGGACTAA 442
QY 361 AACATATTTATGACAGAGAGATATTACAGAGGACATAAAGGCTCAGAACATTTTCTTA 420
DB 443 AACATATTTATGACAGAGAGATATTACAGAGGACATAAAGGCTCAGAACATTTTCTTA 502
QY 421 GCAAGAACGGAATGCTGGCAAGCTTGGGACTTTGGTATAGCAAGAGTCTCGAATAATT 480
DB 503 GCAAGAACGGAATGCTGGCAAGCTTGGGACTTTGGTATAGCAAGAGTCTCGAATAATT 562
QY 481 CCATGGACCTTTCGACCTTGTATTTGGACACACCTTACTCCTGTCGCCAGAGATCTGTC 540
DB 563 CCATGGACCTTTCGACCTTGTATTTGGACACACCTTACTCCTGTCGCCAGAGATCTGTC 622
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QY 661 GTCAAGACACTTTTGCCTCAATATCTCCGGGTTTCTCGTGAGCTCCATCTCTTGATAT 720
DB 743 GTCAAGACACTTTTGCCTCAATATCTCCGGGTTTCTCGTGAGCTCCATCTCTTGATAT 802
QY 721 CTCAGCTCTTTCAAGTATCTCTCGAGACCGACCATCCATAAATTCATTTGAAAGGC 780
DB 803 CTCAGCTCTTTCAAGTATCTCTCGAGACCGACCATCCATAAATTCATTTGAAAGGC 862
QY 781 CCTTTTAGAGAATCTTATCCCAATATTTGACTCTGAGGTCATTCAGGAAGATTCA 840
DB 863 CCTTTTAGAGAATCTTATCCCAATATTTGACTCTGAGGTCATTCAGGAAGATTCA 922
QY 841 GTCACATGCTTATATGACAGACGAGCGCAGCTTCTCGACATGTCTGGAAAGTGTCTC 900
DB 923 GTCACATGCTTATATGACAGACGAGCGCAGCTTCTCGACATGTCTGGAAAGTGTCTC 982
QY 901 AGAAGTGTAAATACAAAAGTGAATTCGGGGAAGTCCCAACCAAGATCAGGATAT 960
DB 983 AGAAGTGTAAATACAAAAGTGAATTCGGGGAAGTCCCAACCAAGATCAGGATAT 1042
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DB 1103 CCCAGAGCCAGATCTTATAAATATGATAGAAAGACCAAAATTTGCTGTCTGTGGAC 1162
QY 1081 ATTTATGATTTATTTATCTCACTTGATATGCTGAGGAGAGAGGCCCAAAACCAAGTT 1140
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QY 1141 ATCACCTTATCTCTCAAGAAATATCTGGAGTTGAGGATTACGGTCAGAAACGAGGCATG 1200
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QY 1201 GTCCATCCCAAGTCAATGG 1220
DB 1283 GTCCATCCCAAGTCAATGG 1302

RESULT 2
BX350584/c
LOCUS
DEFINITION
  BX350584 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
  Homo sapiens cDNA clone CS0DL005YK18 3-PRIME, mRNA sequence.
ACCESSION
  BX350584
VERSION
  BX350584.1 GI:30379530
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 890)
  Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
  Full-length cDNA libraries and normalization
  Unpublished (2001)
REFERENCE
  Contact: Genoscope
  Genoscope - Centre National de Sequencage
  BP 191 91006 Evry cedex - France
  Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
  1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
  end enriched double-strand cDNA was digested with Not I and cloned
  into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
  was normalized. Library was constructed by Life technologies, a
  division of invitrogen. This sequence belongs to sequence cluster
  6942.r,
  and it belongs to a clone representative of this cluster. For more
  information about this cluster and the virtual cDNA, see
  http://www.genoscope.cns.fr/cdna?s=CS0BAI043ZAI1_CS04113_1&c=6942.r

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    25-NORMALIZED"
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    primer. Five prime end enriched, double-strand cDNA was
    digested with Not I and cloned into the Not I and EcoR V
    sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
  Query Match 35.5%; Score 842.2; DB 5; Length 890;
  Best Local Similarity 98.2%; Pred. No. 9.5e-200;
  Matches 872; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

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QY 325 TCTCTCGGTGGTTTGTACAGATTTCTTAGGACTAAACATATTTCTAGCAGAGGATAT 384
DB 831 TCTCTCGGTGGTTTGTACAGATTTCTTAGGACTAAACATATTTCTAGCAGAGGATAT 772
QY 385 TACACAGGACATAAAGCTCAGAACATTTTCTTAGCAAGACGGAATGTGCGCAAGC 444
DB 771 TACACAGGACATAAAGCTCAGAACATTTTCTTAGCAAGACGGAATGTGCGCAAGC 712
QY 445 TTGCGGACTTTGGTATAGCAAGAGTCCTGAATAATTCATGGAACCTTCTCGAACTTGT 504
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Db 711 TTGGGACTTTGGTAGCAAGAGCTCTGAATAATTCATGGAACCTTCTCGAATCTGTA 652
QY 505 TTGGAAACACTTACCTACCTGTCCAGAGATCTGTGAGAAATTAACCCCTACAAATAAAA 564
Db 651 TTGGAAACACTTACCTACCTGTCCAGAGATCTGTGAGAAATTAACCCCTACAAATAAAA 592
QY 565 CGGATATTTGGTCTCTTGGCTGTCTATATAGCTGTGCACACTTAAACATCTTTTG 624
Db 591 CGGATATTTGGTCTCTTGGCTGTCTATATAGCTGTGCACACTTAAACATCTTTTG 532
QY 625 AGGTAACAACTACAGAGCTGGTGTGAAGATTGTCAAGCAATTTGCCCAATAT 684
Db 531 AGGTAACAACTACAGAGCTGGTGTGAAGATTGTCAAGCAATTTGCCCAATAT 472
QY 685 CTCGGGGTTTCTCGTAGCTCCATCTTCAATATCTCAGCTCTTCAAGTATCTCTC 744
Db 471 CTCGGGGTTTCTCGTAGCTCCATCTTCAATATCTCAGCTCTTCAAGTATCTCTC 412
QY 745 GAGCCGACCATCCATAATTCATTTGAAAAGGCCCTTTTGAAGAAATCTTATTC 804
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QY 1045 TGATAGAAAGACCCAAATTTGCTGTCTGTGGACATTTATGATTTATTTATGCTCAAC 1104
Db 111 TGATAGAAAGACCCAAATTTGCTGTCTGTGGACATTTATGATTTATTTATGCTCAAC 52
QY 1105 TTGATATCTGAGGAGGAGCCCAACCAAGTATACCCCTATTC 1152
Db 51 TTGATATGCT-AGGAGGAGAGCCCAACCAAGTATACCCCTATTC 5

RESULT 3
EX342707
LOCUS
DEFINITION
EX342707 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens cDNA clone CS0DL005YK18 5-PRIME, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

EX342707 980 bp mRNA linear EST 08-APR-2004
EX342707 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens cDNA clone CS0DL005YK18 5-PRIME, mRNA sequence.
EX342707
EST.
GI:46279550
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 980)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 2, 2003 this sequence version replaced gi:30344086.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched double-strand cDNA was digested with NotI and cloned
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster

6942.r,
and it belongs to a clone representative of this cluster. For more
information about this cluster and the virtual cDNA, see
http://www.genoscope.cns.fr/cdna?s=CS0DL005BF09P1&c=6942.r.

FEATURES

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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
25-NORMALIZED"
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primer. Five prime end enriched, double-strand cDNA was
digested with NotI and cloned into the NotI and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 34.8%; Score 825.6; DB 5; Length 980;
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QY 660 TGTGAGCAGATTTTCCGCCAATATCTCCGGGGTTTCTCGTAGAGCTCCTTCTTGA 719
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insert sequence.
ACCESSION AK054168
VERSION   AK054168.1 GI:26344040
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          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS  Carninci,P. and Hayashizaki,Y.
TITLE    High-efficiency full-length cDNA cloning
JOURNAL  Meth. Enzymol. 303, 19-44 (1999)
MEDLINE  99279253
PUBMED   10349636
REFERENCE 2
AUTHORS  Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE    Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL  Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE  20499374
PUBMED   11042159
REFERENCE 3
AUTHORS  Shibata,K., Itoh,M., Aizawa,K., Nagao,K., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Katsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yanamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE    RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL  Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE  20530913
PUBMED   11076861
REFERENCE 4
AUTHORS  The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE    Functional annotation of a full-length mouse cDNA collection
JOURNAL  Nature 409, 685-690 (2001)
MEDLINE  11076861
REFERENCE 5
AUTHORS  The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE    Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL  Nature 420, 563-573 (2002)
MEDLINE  12041343
REFERENCE 6
AUTHORS  Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
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Sano,H., Sasaki,D., Shibata,K., Shibata,K., Shinagawa,A., Shiraki,T.,
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Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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RESULT 5
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enriched library, clone:653041J22 product:weakly similar to
protein kinase nek1 (EC 2.7.1.1-) [Mus musculus], full insert
sequence.
ACCESSION
AK032672
VERSION
AK032672.1 GI:26328482
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
2
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REFERENCE
AUTHORS

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, I., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multipillar sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

4 The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 585-590 (2001)

JOURNAL
AUTHORS

5 The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL
REFERENCE
AUTHORS

6 (bases 1 to 2407)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
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Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission

JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.

FEATURES
source

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Best Local Similarity 81.1%; Pred. No. 2.9e-138;
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DEFINITION Homo sapiens HCM2274 gene, VIRTUAL TRANSCRIPT, partial sequence,
ACCESSION AY405588
VERSION AY405588.1 GI:39761562
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SOURCE Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 603)
AUTHORS: Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrieza,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 603)
AUTHORS: Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrieza,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submisison
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
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Query Match 25.1%; Score 594; DB 9; Length 603;
Best Local Similarity 99.2%; Pred. No. 1.5e-137;
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QY 231 GCGAGCTGTTTATTGTAATGGAATATTGTGATGAGGGATCTCATGAAAGGATCAAT 290
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QY 351 CTAGGACTTAAACATATTCATGACAGGAGATATTACACAGGACATATAAGCTCAGAAC 410
DB 121 CTAGGACTTAAACATATTCATGACAGGAGATATTACACAGGACATATAAGCTCAGAAC 180
QY 411 ATTTTCTTAGCAAGAACCGAATGTTGGCAAGCTTTGGGACTTTGGTATAGCAAGATC 470
DB 181 ATTTTCTTAGCAAGAACCGAATGTTGGCAAGCTTTGGGACTTTGGTATAGCAAGATC 240
QY 471 CTGAATAATTCATGGAACCTTCTCGAAGCTTGTATTGGAACACCTTACTACTGTCCTCA 530
DB 241 CTGAATAATTCATGGAACCTTCTCGAAGCTTGTATTGGAACACCTTACTACTGTCCTCA 300
QY 531 GAGATCTGTGAGATAAACCCTTACAAACATATAAAGGATATTGTTGTTCTCTTTGGTGTGTC 590

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Db      301  |||||GAGATCTGTGAGAAATTAACCCCTACACAAATATAAAGCATATTTGGTCTCTTGGCTGTGTC 360
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Qy      651  |||||CTGAAGATTGTCAAGCACATTTTCCCAATATCTCCGGGGTCTTTCTCGTGAGCTCCAT 710
Db      421  |||||CTGAAGATTGTCAAGCACATTTTCCCAATATCTCCGGGGTCTTTCTCGTGAGCTCCAT 480
Qy      711  |||||TCCTTGATATCTCAGCTCTTCAAGTATCTCTCGAGCCGACCATCCATAAATTCATTT 770
Db      481  |||||TCCTTGATATCTCAGCTCTTCAAGTATCTCTCGAGCCGACCATCCATAAATTCATTT 540
Qy      771  |||||TTGAAAGGCCCTTTTGTAGGAATCTTATTCCCAATATTTGACTCTCTGAGGTCAATTCAG 830
Db      541  |||||TTGAAAGGCCCTTTTGTAGGAATCTTATTCCCAATATTTGACTCTCTGAGGTCAATTTT 600
Qy      831  GA 832
Db      601  GA 602

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RESULT 7

BX417448
 LOCUS BX417448 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE009YJ07
 DEFINITION 5-PRIME, mRNA sequence.

ACCESSION

BX417448
 VERSION BX417448.2 GI:46926799

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 872)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)

TITLE

On May 13, 2003 this sequence version replaced gi:30642067.

COMMENT

Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with NotI and cloned
 into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 6942.r
 There is a virtual cDNA representing this cluster. For more
 information about this cluster and the virtual cDNA, see
 http://www.genoscope.cns.fr/cdnas=CS0DE009CE04QP1&c=6942.r.
 Location/Qualifiers

FEATURES

source

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 /clone_lib="Homo sapiens PLACENTA"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with NotI and cloned into
 the NotI and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."

ORIGIN

Query Match 24.3%; Score 574.8; DB 5; Length 872;
 Best Local Similarity 84.1%; Pred. No. 1.1e-132;
 Matches 695; Conservative 1; Mismatches 123; Indels 7; Gaps 4;

215 TTCAATTTCAAGAGAAATGCGAGGCTGTTTATTGTAATGGAATATTGTGATGAGGGATCT 274
 Db 51 TTTTCTTACAGAGAAATGCGAGGCTGTTTATTGTAATGGAATATTGTGATGAGGGATCT 110
 Qy 275 CATGAAAAGGATCAATAGACAAACGGGGTGTATTATTAGTGAAGATCAGATCTCTCGGTG 334
 Db 111 CATGAAAAGGATCAATAGACAAACGGGGTGTATTATTAGTGAAGATCAGATCTCTCGGTG 170
 Qy 335 GTTTGTACAGATTCTCTAGGACTTAAACATATTTCATGACAGGAAGATATTACACAGGA 394
 Db 171 GTTTGTACAGATTCTCTAGGACTTAAACATATTTCATGACAGGAAGATATTACACAGGA 230
 Qy 395 CATAAAAGCTCAGAACATTTTCTTAGCAAGACGGAATGGTGGCAAGCTTGGGACTT 454
 Db 231 CATAAAAGCTCAGGTAAACAGCTCAGAGAGAAGACTAAGACAGAACTGATCTTTTCTTGA 290
 Qy 455 TGGTATAGCAGAGTCTCTGATTAATCCATGGAACTTGTCTGAACTTGTTATTGGAACACC 514
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 Qy 515 TTACTACTGTGCCCGAGAGATCTGTGAGAAATAAACCCCTACAACTAAACCGGATATTG 574
 Db 351 ATGCTGGCAAGCTTGGGACTT---TGGTATAGCAAGAGTCTCTGAATAAGGATATTG 406
 Qy 575 GTCTCTTGGCTGTGCTCTATATGAGCTCTGCACACTTAAACATCTTTTGGAGGTAAACA 634
 Db 407 GTCTCTTGGCTGTGCTCTATATGAGCTCTGCACACTTAAACATCTTTTGGAGGTAAACA 466
 Qy 635 CTTACAGCAGCTGTTCTGAAGATTGTGCAAGCACATTTTGCCTCAATATCTCCGGGGTT 694
 Db 467 CTTACAGCAGCTGTTCTGAAGATTGTGCAAGCACATTTTGCCTCAATATCTCCGGGGTT 526
 Qy 695 TTCTGTGAGCTCAATCTCTTGATATCTGAGTCTTTTCAAGTATCTC-CTCGAGACCGAC 753
 Db 527 TTCTGTGAGCTCAATCTCTTGATATCTGAGTCTTTTCAAGTATCTC-CTCGAGACCGAC 586
 Qy 754 CATCCATAAATTCATTTTCAAAAGGCCCTTTTGTAGAGATCTTATTTCCCAATATTGGA 813
 Db 587 CATCCATAAATTCATTTTCAAAAGGCCCTTTTGTAGAGATCTTATTTCCCAATATTGGA 646
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 Db 647 CTCTGAGGTCAATTCAGGAAGAAATTCAGTCAATGCTTATATCCAGACGAGGACCCAG 706
 Qy 874 CTTCTGCACATCTGGGAGGTGTCAGAGAGTAAATATCAAAAGAGTGAATTCCTCGG 932
 Db 707 CTTCTGCACATCTGGGAGGTGTCAGAGAGTGAATATCAAAAGAGTGAATTCCTCGG 766
 Qy 933 GGAAGTGGCCACCAAGATCAAGGATATCTGTGCCAATTAAGAGGATGCTATATTGCAT 992
 Db 767 GGAAGTGGCCACCAAGATCAAGGATATCTGTGCCAATTAAGAGGATGCTATATTGCAT 826
 Qy 993 AGAAATGAATGGAGACACACAGCTGGAGCCCGAGAGCCAGATCTTA 1038
 Db 827 AGAAATGAATGGAGA-CMCCAGCTGGAGCCGAGGAAGGAGATCTATA 871

RESULT 8

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

UNPUBLISHED

EST

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 670)

Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and

Zeng, Y.-X.

Transcriptional Gene Expression Profile of Human Nasopharynx

Unpublished (2003)

COMMENT

Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.

FEATURES

Location/Qualifiers
source
1..670
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match 23.1%; Score 547.8; DB 6; Length 670;
Best Local Similarity 99.6%; Pred. No. 5.9e-126;
Matches 549; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CATTGGAGACCATGATAAGTACCATGTGATTAGGCCATCGGCCAAGGTGCCTTCGGGA 60
DB 105 CATTGGAGACCATGATAAGTACCATGTGATTAGGCCATCGGCCAAGGTGCCTTCGGGA 164
QY 61 AAGCATACTTACGTAAGGGGAATCAGATAGCAAGCACTGTGTCAATAAAGAGATCAATT 120
DB 165 AAGCATACTTACGTAAGGGGAATCAGATAGCAAGCACTGTGTCAATAAAGAGATCAATT 224
QY 121 TTGAAGAATGCCATACAGAAAGAAAGAGCTTCAAGAAAGAGAGTCAATTCCTCGAAA 180
DB 225 TTGAAGAATGCCATACAGAAAGAAAGAGCTTCAAGAAAGAGAGTCAATTCCTCGAAA 284
QY 181 AGATGAACATCCCAACATTTGTAGCCTTCTTCAATTCATTTCAAGAGATGGCAGGCTGT 240
DB 285 AGATGAACATCCCAACATTTGTAGCCTTCTTCAATTCATTTCAAGAGATGGCAGGCTGT 344
QY 241 TTATGTAAATCGAATATTTGATCGAGGGATCTCATGAAAGAGATCAATAGACACGGG 300
DB 345 TTATGTAAATCGAATATTTGATCGAGGGATCTCATGAAAGAGATCAATAGACACGGG 404
QY 301 GTGTGTTATTTAGTGAAGATCAGATCCTCGGTGGTTGTACAGATTTCTTAGGACTAA 360
DB 405 GTGTGTTATTTAGTGAAGATCAGATCCTCGGTGGTTGTACAGATTTCTTAGGACTAA 464
QY 361 AACATATTCATGACAGGAAGATATTACAGGGACATATAAAGCTCAGAACATTTTCTTA 420
DB 465 AACATATTCATGACAGGAAGATATTACAGGGACATATAAAGCTCAGAACATTTTCTTA 524
QY 421 GCAAGAACGGAATGGTGGCAAGCTTGGGACTTTGGTATAGCAAGAGTCTCTGAATAATT 480
DB 525 GCAAGAACGGAATGGTGGCAAGCTTGGGACTTTGGTATAGCAAGAGTCTCTGAATAATT 584
QY 481 CCATGGAACTTGTCTGAACTTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCTGTC 540
DB 585 CCATGGAACTTGTCTGAACTTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCTGTC 644
QY 541 AGAATAAACCC 551
DB 645 AGAATAAACCC 655

RESULT 9

BQ917635
LOCUS BQ917635
DEFINITION AGENCOURT_888753 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6311513
5', mRNA sequence.
ACCESSION BQ917635
VERSION BQ917635.1 GI:22332333
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

1 (bases 1 to 928)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Susan L. Sullivan, PhD.

cDNA Library Preparation: ResGen, Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM13735 row: i column: 18

High quality sequence stop: 734.

Location/Qualifiers

source

1..928

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:6311513"

/lab host="DH10B (phage-resistant)"

/clone lib="NIH MGC 129"

/note="Organ: olfactory epithelium; Vector: pCMV-SPORT6.1;

Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally.

Primer: Oligo dt. Average insert size 2.2 kb. Constructed

by ResGen, Invitrogen Corp. Note: this is a NIH_MGC

Library."

ORIGIN

Query Match 21.8%; Score 516.8; DB 5; Length 928;
Best Local Similarity 81.2%; Pred. No. 3.8e-118;
Matches 642; Conservative 0; Mismatches 133; Indels 16; Gaps 3;
QY 10 CCATGGATAAGTACGATGTGATTAGGCCATCGGCCAAGGTGCCTTCGGGAAAGCATACT 69
DB 91 CCATGGATAAGTACGATGTGATTAGGCCATCGGCCAAGGTGCCTTCGGGAAAGTACT 150
QY 70 TAGCTAAAGGGAATCAGATAGCAAGCACTGTGTCAATAAAGAGATCAATTTGAAAGA 129
DB 151 TGCTTAAAGATAAATCAGAAAGCACTGTGTCAATAAAGAGATCAATTTGCAAG- 209
QY 130 TGCCCATACAGAAAGAAAGAGCTTCAAGAAAGAGTGAATCTTCTGAAAGATGAAC 189
DB 210 -----GAAAGAGGCTTCAAGAGAGTGAATCTTCTGCTAGGATGGAGC 258
QY 190 ATCCCAACATTTAGCTTCTTCAATTCATTTCAAGAGATGGCAGGCTGTTATTGTAA 249
DB 259 ATCCCAATATCGTAACCTTCTTCAGCTCGTTTCAAGAGAGCGGAGGCTGTTATTGTAA 318
QY 250 TGGATATTTGATGAGGAGGATCTCATGAAAGAGATCAATAGCAACGGGTGTGTTAT 309
DB 319 TGGATATTTGATGAGGAGGATCTCATGAGAGATCCAGAGGAGCGGGAGTGTATG 378
QY 310 TTAGTGAAGATCAGATCCTCGGTGGTTGTGTACAGATTTCTTAGGACTAAACATATTC 369
DB 379 TCAGCGAAGACCCAGATCCTGTGTTGTTGTACAGATTTCTTAGGACTGAAGCATATTC 438
QY 370 ATCAGAGGAGATATTACAGAGGACATAAAGCTCAGAACATTTTCTTAGCAAGACG 429
DB 439 ATGACAGGAAGATTTTACAGAGGACATAAATCTCAGATATTTTCTTAGCAAGATG 498
QY 430 GAATGGTGGCAAGCTTGGGACTTTGGTATAGCAAGAGTCTCGAATAATTTCCATGGAAC 489
DB 499 GAATGGTGGCAAGCTTGGGACTTTGGAAACAGCAAGACACTGAATGACTCCATGGAAC 558
QY 490 TTGCTCGAAGCTTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCTGTGAGATAAAC 549
DB 559 TTGCTCAAAACATGTCTGTGGACACCTTACTACCTGTCCCCAGAGATCTGTGAGACAGGC 618
QY 550 CCTACAAACAATAAAGCGGATATTTGGTCTCTTGGCTGTGTCTTATATAGCTCTGCACAC 609

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Db      619 CATACACATAAAACCGGACATCTGGTCTCTGGGTGTGTCTATATGAGCTCTGCACAC 678
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Db      679 TCAAGCATCTTTTGAAGAGCAACAACCTCCACCATCTGGTCTGAAGATTGTCAAGGAC 738
QY      670 ATTTCGCCCAATATCTCGGGGTTTCTCGTAGCTCCATCC--TTGATATCTCAGCT 727
Db      739 GTGTTCTCCCATATCACCCCACTTCTCTCGTAGCTACAGTNCCTTGATACCTCAGCT 798
QY      728 CTTTCAAGTATCTCTCCGAGACC--GACCATCCATAAATTCATTTTGAAGAGGCCCTTT 785
Db      799 CTTCAAGTGTCTCTCAGAGCCGCGCATCGTTACGTCCCTTTTGAAGAGCCCTTT 858
QY      786 TTAGAGAACTCT 796
Db      859 TTTTAGAAACT 869

CD243608      856 bp      mRNA      linear      EST 22-MAY-2003
LOCUS      AGENCOURT_14121106 NIH_MGC_180 Homo sapiens cDNA clone
DEFINITION      IMAGE:30383658 5', mRNA sequence.
ACCESSION      CD243608
VERSION      EST.
KEYWORDS      CD243608.1 GI:31004072
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL      NIH-MGC http://mgs.nci.nih.gov/
COMMENT      National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM447 row: n column: 19
High quality sequence stop: 545.
FEATURES      Location/Qualifiers
Source      1..856
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            /lab_host="DH10B-Tcn A ( T1 and T5 phage resistances)"
            /clone_lib="NIH_MGC_180"
            Note="Organ: Testis; Vector: pCMV-SPORT6.1; Site 1: NotI;
            Site 2: EcoRV (destroyed); Library is oligo-dT primed and
            directionally cloned (EcoRV site is destroyed upon
            cloning). Average insert size 1.68 kb. Library was
            constructed by (Invitrogen). Note: this is a NIH_MGC
            Library."

ORIGIN
Query Match      20.5%; Score 485; DB 6; Length 856;
Best Local Similarity 94.3%; Pred. No. 3.5e-110;
Matches 548; Conservative 0; Mismatches 25; Indels 8; Gaps 4;

QY      1 CATTGAGACCATGGATAGTACGATGCTATTAAAGCCATCGGCAAGTGCCTTCGGGA 60
Db      137 CATTGAGACCATGGATAGTACGATGCTATTAAAGCCATCGGCAAGTGCCTTCGGGA 196
QY      61 AAGCATCTTAGCTAAAGGAATCAGATAGCAAGCACTGTGTCTATAAAGAGATCAATT 120

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Db      197 AAGCATCTTAGCTAAAGGGAAATCAGATAGCAAGCACTGTGTCTATAAAGAGATCAATT 256
QY      121 TTGAAAAGATGCCCATACAGAAAAGAAGCTTCAAAAGAAAAGATGATCTTCTCTGAAA 180
Db      257 TTGAAAAGATGCCCATACAGAAAAGAAGCTTCAAAAGAAAAGATGATCTTCTGAAA 316
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Db      317 AGATGAACATCCCAACATTGTAGCCTTCTCAATTCAATTTCAAGAGAATGGCAGGCTGT 376
QY      241 TTATTGTAATGGAAATATTGTGATGGAGGGATCTCATGAAAAGGATCAATAGACAACGGG 300
Db      377 TTATTGTAATGGAAATATTGTGATGGAGGGATCTCATGAAAAGGATCAATAGACAACGGG 436
QY      301 GTGTGTTATTAGTGAAGATCAGATCCTCGTGGTGGTTGTGTACAGATTTCTCTAGGACTAA 360
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QY      361 AACATATTATGACAGGAAGATATTACACAGGGACATATAAAGCTCAGAACATTTTCTTA 420
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Db      557 GTCAGAACGGAATGGTGGCAAGCTTGGGACCTTTGGTATAGCAAGAGTCCCTGAATAAT 616
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Db      617 TCCATGGGAACTTGTCTGAACTTGTATTTGGGAACACCTTTACTACCTGTGCCCCAGAAGA 676
QY      533 GATCTGTGAGATAAACCCTACCAACATAAAGCGATATT 573
Db      677 TCTGTTCAGATAAACCCTACCAACATAAAGCGGATAT 717

RESULT 11
LOCUS      AY405589
DEFINITION      Pan troglodytes HCM2274 gene, VIRTUAL TRANSCRIPT, partial sequence,
ACCESSION      AY405589
VERSION      AY405589.1 GI:39761563
KEYWORDS      GSS.
SOURCE      Pan troglodytes (chimpanzee)
ORGANISM      Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE      1 (bases 1 to 603)
            Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
            Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
            Science 302 (5652), 1960-1963 (2003)
JOURNAL      14671302
PUBMED      2 (bases 1 to 603)
REFERENCE      Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
            Direct Submission
            Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
            This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES      Location/Qualifiers
Source      1..603
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ORIGIN
Query Match      19.6%; Score 464.8; DB 9; Length 603;
Best Local Similarity 77.9%; Pred. No. 3.7e-105;
Matches 469; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 231 GCGAGGCTGTTTATTGTAATGGAATATTGTGATGGAGGGATCTCATGAAAGGATCAAT 290
DB 1 GCGAGGCTGTTTATTGTAATGGAATATTGTGATGGAGGGATCTCATGAAAGGATCAAT 60

QY 291 AGACAAAGGGGTGTTTATTGTAATGGAATATTGTGATGGAGGGATCTCATGAAAGGATCAAT 350
DB 61 AGACAAAGGGGTGTTTATTGTAATGGAATATTGTGATGGAGGGATCTCATGAAAGGATCAAT 120

QY 351 CTAGAGCTTAAACATATTATTCATGACAGGAGATATTACACAGGGACATATAAGCTCAGAAC 410
DB 121 CTAGAGCTTAAACATATTATTCATGACAGGAGATATTACACAGGGACATATAAGCTCAGAAC 180

QY 411 ATTTTCTTCTAGCAAGAACGGAAATGTTGTAATGGAATATTGTGATGGAGGGATCTCATGAAAGGATCAAT 470
DB 181 ATTTTCTTCTAGCAAGAACGGAAATGTTGTAATGGAATATTGTGATGGAGGGATCTCATGAAAGGATCAAT 240

QY 471 CTAGAGCTTAAACATATTATTCATGACAGGAGATATTACACAGGGACATATAAGCTCAGAAC 530
DB 241 CTAGAGCTTAAACATATTATTCATGACAGGAGATATTACACAGGGACATATAAGCTCAGAAC 600

QY 531 GAGATCTCTCAGAAATAAAACCTTACAAACATATAAGCTTGGTCTCTTGGTCTGTGTC 590
DB 301 GAGATCTCTCAGAAATAAAACCTTACAAACATATAAGCTTGGTCTCTTGGTCTGTGTC 360

QY 591 TTATATGAGCTCTGCACACTTAAACATCTTTTGGAGGGTAAACATTTACAGCAGCTGGTT 650
DB 361 TTATATGAGCTCTGCACACTTAAACATCTTTTGGAGGGTAAACATTTACAGCAGCTGGTT 420

QY 651 CTGAAGATTGTCAGACACATTTTCCCAATATCTCCGGGTTTTCCTCGTGAGCTCCAT 710
DB 421 CTGAAGATTGTCAGACACATTTTCCCAATATCTCCGGGTTTTCCTCGTGAGCTCCAT 480

QY 711 TCCTTGATATCTCAGCTCTTCAAGTATCTCTCGAGACCGACCATCCATAAATTCATT 770
DB 481 TCCTTGATATCTCAGCTCTTCAAGTATCTCTCGAGACCGACCATCCATAAATTCATT 540

QY 771 TTGAAGAGCCCTTTTGAAGATCTTATCCCAATATTGCTCTGAGGTCATTGAG 830
DB 541 TTGAAGAGCCCTTTTGAAGATCTTATCCCAATATTGCTCTGAGGTCATTGAG 600

QY 831 GA 832
DB 601 GA 602

RESULT 12
AY405590 603 bp DNA linear GSS 12-DEC-2003
LOCUS Mus musculus HCM2274 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY405590
VERSION AY405590.1 GI:39761564
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
source 1..603
/organism="Mus musculus"
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ORIGIN
Query Match      19.2%; Score 455.4; DB 9; Length 603;
Best Local Similarity 84.9%; Pred. No. 8.5e-103;
Matches 510; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 231 GCGAGGCTGTTTATTGTAATGGAATATTGTGATGGAGGGATCTCATGAAAGGATCAAT 290
DB 1 GCGAGGCTGTTTATTGTAATGGAATATTGTGATGGAGGGATCTCATGAGAGATCCAG 60

QY 291 AGACAAAGGGGTGTTTATTGTAATGGAATATTGTGATGGAGGGATCTCATGAAAGGATCAAT 350
DB 61 AGGACAGGGGGATGATGTTTCAGGAGAACAGCATCTGTGTTGGTTGTACAGATTCT 120

QY 351 CTAGAGCTTAAACATATTATTCATGACAGGAGATATTACACAGGGACATATAAGCTCAGAAC 410
DB 121 CTAGAGCTTAAACATATTATTCATGACAGGAGATATTACACAGGGACATATAAGCTCAGAAT 180

QY 411 ATTTTCTTCTAGCAAGAACGGAAATGTTGTAATGGAATATTGTGATGGAGGGATCTCATGAAAGGATCAAT 470
DB 181 ATTTTCTTCTAGCAAGAACGGAAATGTTGTAATGGAATATTGTGATGGAGGGATCTCATGAAAGGATCAAT 240

QY 471 CTGAATATTTCATGAGAACTTCTCGAATCTTGTGATTTGGAAACAGCAAGAAC 530
DB 241 CTGAATATTTCATGAGAACTTCTCGAATCTTGTGATTTGGAAACAGCAAGAAC 300

QY 531 GAGATCTCTCAGAAATAAAACCTTACAAACATATAAGCTTGGTCTCTTGGTCTGTGTC 590
DB 301 GAGATCTCTCAGAAATAAAACCTTACAAACATATAAGCTTGGTCTCTTGGTCTGTGTC 360

QY 591 TTATATGAGCTCTGCACACTTAAACATCTTTTGGAGGGTAAACATTTACAGCAGCTGGTT 650
DB 361 TTATATGAGCTCTGCACACTTAAACATCTTTTGGAGGGTAAACATTTACAGCAGCTGGTT 420

QY 651 CTGAAGATTGTCAGACACATTTTCCCAATATCTCCGGGTTTTCCTCGTGAGCTCCAT 710
DB 421 CTGAAGATTGTCAGACACATTTTCCCAATATCTCCGGGTTTTCCTCGTGAGCTCCAT 480

QY 711 TCCTTGATATCTCAGCTCTTCAAGTATCTCTCGAGACCGACCATCCATAAATTCATT 770
DB 481 TCCTTGATATCTCAGCTCTTCAAGTATCTCTCGAGACCGACCATCCATAAATTCATT 540

QY 771 TTGAAGAGCCCTTTTGAAGATCTTATCCCAATATTGCTCTGAGGTCATTGAG 830
DB 541 TTGAAGAGCCCTTTTGAAGATCTTATCCCAATATTGCTCTGAGGTCATTGAG 600

QY 831 G 831
DB 601 G 601

RESULT 13
BB666328 659 bp mRNA linear EST 26-OCT-2001
LOCUS BB666328 RIKEN full-length enriched, 2 days pregnant adult female
DEFINITION ovary Mus musculus cDNA clone E330012F19 5', mRNA sequence.
ACCESSION BB666328

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VERSION          BB566328.1  GI:16499961
KEYWORDS
SOURCE           Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS          Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
                 Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
                 Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
                 Ono,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
                 Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
                 Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
                 Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE            RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL          Unpublished (2001)
COMMENT          Contact: Yoshihide Hayashizaki
                 Laboratory for Genome Exploration Research Group, RIKEN Genomic
                 Sciences Center(GSC), Yokohama Institute
                 The Institute of Physical and Chemical Research (RIKEN)
                 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                 Tel: 81-45-503-9222
                 Fax: 81-45-503-9216
                 Email: genome-resgsc.riken.jp, URL:http://genome.gsc.riken.jp/
                 Carninci,P., Shibata,K., Hayatsu,N., Sugahara,Y., Shibata,K.,
                 Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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                 prepare full-length cDNA libraries for rapid discovery of new
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                 10 (11), 1757-1771 (2000)
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                 Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                 Hayashizaki,Y.
                 Computational Analysis of Full-Length Mouse cDNAs Compared with
                 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                 Please visit our web site (http://genome.gsc.riken.go.jp) for
                 further details.
FEATURES         e mouse tissues.
                 Location/Qualifiers
                 1..659
                 /organism="Mus musculus"
                 /mol_type="mRNA"
                 /db_xref="taxon:10090"
                 /clone="E330012F19"
                 /sex="female"
                 /tissue_type="ovary"
                 /dev_stage="2 days pregnant adult"
                 /lab_host="PH10B"
                 /clone_lib="RIKEN full-length enriched, 2 days pregnant
                 adult female ovary"
                 /note="Site 1: Sali; Site 2: BamHI; cDNA library was
                 prepared and sequenced in Mouse Genome Encyclopedia
                 Project of Genome Exploration Research Group in Riken
                 Genomic Sciences Center and Genome Science Laboratory in
                 RIKEN, Division of Experimental Animal Research in Riken
                 contributed to prepare mouse tissues. 1st strand cDNA was
                 primed with a primer [5',
                 GAGAGAGAGCGCGCAACTTTTTTTTTTTTNN 3'], cDNA was
                 prepared by using trehalose thermo-activated reverse
                 transcriptase and subsequently enriched for full-length by
                 cap-trapper. Second strand cDNA was prepared with the
                 primer adaptor of sequence [5'

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ORIGIN
Query Match      19.1%; Score 452.4; DB 2; Length 659;
Best Local Similarity 84.8%; Pred No. 4.9e-102;
Matches 507; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
QY 224 AGAAGTGGCAGGCTGTTTATTGTAATGGAATATTGTGATGGAGGGGATCTCATGAAAAG 283
DB 53 AGAGAAGCGCAGGCTGTTTATTGTAATGGAATACTGTGATGGAGGGGATCTCATGAGAG 112
QY 284 GATCAATAGACAACGGGGTGTGTTATTAGTAGAGATCAGATCTCCGGTGGTGTGTAC 343
DB 113 GATCCAGAGGCGGGGAGTGATGTTTCAGGAAGACAGATCTGTGTGGTGTGTAC 172
QY 344 GATTTCCTAGAGCTAAAACATATTTCATGACAGGAAGATATTACACAGGAGCATATAAAGC 403
DB 173 GATTTCCTAGAGCTGAAGCATATTTCATGACAGGAAGATTTTACACAGGAGCATATAATC 232
QY 404 TCAGAACATTTTTCTTAGCAAGAACGGGAATGGTGGCAAGCTTGGGGACTTTGGTATAGC 463
DB 233 TCAGAAATATTTTCTTAGCAAGATGGATGGTTGCCAAGCTCGGGGACTTTGGAAACAGC 292
QY 464 AAGAGTCTGTAATAATTCATGGAACCTTGTCTCGAATCTGTATTGGAACACCTTACTACCT 523
DB 293 AAGAACACTGATGATCCATCCAGAACTTGTCTCAAAATGCTGTGGACACCTTACTACCT 352
QY 524 GTCCCCAGAGATCTGTGAGAAATAAACCTTACAAATAAAGCGGATATTTGGTCTCTGG 583
DB 353 GTCCCCAGAGATCTGTGAGAAACAGGCCATACAAATAAAGCGGACATCTGGTCTCTGG 412
QY 584 CTGTGCTCTTATAGAGCTCTGCACACTTAAACATCCCTTTTGAGGGGTACACACTTACAGCA 643
DB 413 CTGTGCTCTTATAGAGCTCTGCACACTCAAGCATCTTTTGAGAGAGCAACACTTCCACCA 472
QY 644 GCTGGTCTCAAGATTTGTCAAGCACATTTTGCCCCAATATCTCCGGGGTTTTCTCGTGA 703
DB 473 TCTGGTCTCAAGATTTGTCAAGGACGTTGTGCTCCCATATCACCCCACTTCTCTGTA 532
QY 704 GCTCANTCTTGTATCTCAGCTCTTCAAGTATCTCTCGAGAGCCGACATCCATAAA 763
DB 533 CCTACAGTCTTGTATCTCAGCTCTTCAAGTATCTCTCGAGAGCCGACATCCGTTAC 592
QY 764 TTCCATTTTGAAGAGCCCTTTTAGAGAACTCTATTCCCAATATTTGACTCTCTGAG 821
DB 593 GTCCCTTTTGAAGAGCCCTTTTAGAAACTCTCATTTGCCCGATCTCTTGTATCTGAG 650
RESULT 14
BX328262 LOCUS
DEFINITION BX328262 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens cDNA clone CS0DL005YK18 5-PRIME, mRNA sequence.
ACCESSION BX328262
VERSION BX328262.2 GI:46281652
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 678)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 2, 2003 this sequence version replaced gi:30344693.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned

```

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6942.r, and it belongs to a clone representative of this cluster. For more information about this cluster and the virtual cDNA, see http://www.genoscope.cns.fr/cdna?c=CSOBAG5442E01_CS050531&c=6942.r

FEATURES

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Location/Qualifiers
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/mol_type="mRNA"
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/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

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ORIGIN

Query Match	18.8%	Score 446.2	DB 5	Length 678
Best Local Similarity	99.3%	Prod. No. 1.8e-100		
Matches 448	Conservative 0	Mismatches 3	Indels 0	Gaps 0
770	TTTGAAGAGGCCCTTTTATAGAGATCTTATTCCTCCAAATATTGTGACTCTCGAGGTCATTCA	829		
45	TTTTCAAGAGGCCCTTTTATAGAGATCTTATTCCTCCAAATATTGTGACTCTCGAGGTCATTCA	104		
830	GGAAGAAATTCAGTCAATGCTTTATATGCAGACGAGGAGCGCCAGCTTCTCGACATGCTGG	889		
105	GGAAGAAATTCAGTCAATGCTTTATATGCAGACGAGGAGCGCCAGCTTCTCGACATGCTGG	164		
890	GAAAGTGTGTCAGAAAGTGTAAAAATACAAAAGTGCAGATTCCGGCGGAAGTGCCTCCACCAAG	949		
165	GAAAGTGTGTCAGAAAGTGTAAAAATACAAAAGTGCAGATTCCGGCGGAAGTGCCTCCACCAAG	224		
950	ATCAAGGATATCTGTGCGCAATTTAAAGAAATGCTATATTGCATAGAAATGAATGGAGACC	1009		
225	ATCAAGGATATCTGTGCGCAATTTAAAGAAATGCTATATTGCATAGAAATGAATGGAGACC	284		
1010	ACCAGCTGAGCCCAAGAGGCGCAGATCTATAAAAATGATGAAAGACCCCAAAATTTGCTGC	1069		
285	ACCAGCTGAGCCCAAGAGGCGCAGATCTATAAAAATGATGAAAGACCCCAAAATTTGCTGC	344		
1070	TGTCGTGCGACATTAATGATTTATTTATGCTCAACTTGATATGCTGAGGAGGAGGCCCA	1129		
345	TGTCGTGCGACATTAATGATTTATTTATGCTCAACTTGATATGCTGAGGAGGAGGCCCA	404		
1130	CAAAACCAAGTTATCACCTTATTCCTCAAGAAAATACTGGAGTTCAGAGATTACGGTCAAGGA	1189		
405	CAAAACCAAGTTATCACCTTATTCCTCAAGAAAATACTGGAGTTCAGAGATTACGGTCAAGGA	464		
1190	AACGAGGCATGGTCCATCCCCCAAGTCAATGG	1220		
465	AACGAGGCATGGTCCATCCCCCAAGTCAATGG	495		

RESULT 15

BB523078	BB523078	639 bp	mRNA	linear	EST 26-OCT-2001
LOCUS					
DEFINITION	BB523078	RIKEN full-length cDNA clone	BB523078	BB523078	BB523078
ACCESSION	BB523078	BB523078	BB523078	BB523078	BB523078
VERSION	BB523078.1	BB523078.1	BB523078.1	BB523078.1	BB523078.1
KEYWORDS	EST.	EST.	EST.	EST.	EST.
SOURCE	Mus musculus	Mus musculus	Mus musculus	Mus musculus	Mus musculus
ORGANISM	Mus musculus	Mus musculus	Mus musculus	Mus musculus	Mus musculus
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

BamHI "

ORIGIN

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Query Match      16.5%; Score 392; DB 2; Length 639;
Best Local Similarity 82.7%; Pred. No. 6.8e-87;
Matches 465; Conservative 0; Mismatches 85; Indels 12; Gaps 1;

QY 10 CCATGGATAAGTACGATGTGATTAAGGCCATCGGCAAGGTGCGCTTCGGGAAGCATACT 69
Db 90 CCATGGATAACTTCACTGATTAAGATCATTTGGGAAGGCACCTTTGGGAAGGTGCTACT 149

QY 70 TAGCTAAAGGAATCAGATAGCAAGCACGTGTCATATAAGAGATCAATTTTGAAGA 129
Db 150 TGGCTAAAGTAATCAGAAGCAGTCACGTGTCATAAAGAAATCAGTTTGACAAG- 208

QY 130 TGGCCATACAGAAAAGAGCTTCAAGAAAGAGATGATTCTTCTGGAAGAGATGAAAC 189
Db 209 -----GAAAGAGGCTCAAGAACGAGTGATTCITCTGGCTAGATGGAGC 257

QY 190 ATCCCAACATGTAGCTTCTTCAATTCAATTTCAAGAGATGCGAGGCTGTTTATTGTAA 249
Db 258 ATCCCAATATCGTAACCTTCTTCAGCTCGTTTCAAGAGAACGCGAGCTGTTTATTGTAA 317

QY 250 TGAATATTTGATGGAGGGATCTCATGAAAAGGATCAATAGACAAACGGGTGCTTAT 309
Db 318 TGGATACTGTGATGGAGGGATCTCATGAGAGGATCCAGAGGACGGGGAGTGATGT 377

QY 310 TTAGTGAAGATCAGATCCCTCGTTGGTTTGTACAGATTTCTTAGGACTAAACATATTC 369
Db 378 TCAGCGAAGACCAAGATCCTGTGTGTTGTACAGATTTCTTAGGACTGAAGCATATTC 437

QY 370 ATGACAGGAGATATTACACAGGACATATAAGCTCAGAACATTTTCTTAGCAAGAACG 429
Db 438 ATGACAGGAAGATTTTACACAGGACATAAAATCTCAGAAATATTTTCTTAGCAAGATG 497

QY 430 GAATGTGGCAAGCTTTGGGACTTTGGTATAGCAAGAGTCTCTGAATAATTCATGGAAC 489
Db 498 GAATGGTTGCCAAGCTCGGGACTTTGGAACACNAGAACACTGATGACTCCATGGAAC 557

QY 490 TTGCTCGAATTTGTATTGGAACACCTTACTACTGTCCTCCAGAGATCTGTCTAGATAAAC 549
Db 558 TTGCTCAACATGTGTGGACACCTTACTACTGTCCTCCCAAGATCTGGCAGAACAGGC 617

QY 550 CCTACAAACAATAAAACGGATAT 571
Db 618 CATACAAACAATAAAACGGACAT 639
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